



1/66

```
1  AAAATGTATG GATACAACTT ACGTTTGATG AAAGATTTGG GCTTGAAGAC CCAGAAGATG
   TTTTACATAC CTATGTTGAA TGCAAACTAC TTTCTAAACC CGAACTTCTG GGTCTTCTAC

61  ACATATGCAA GTATGATTTT GTAGAAGTTG AGGAACCCAG TGATGGAAC TATTAGGGC
   TGTATACGTT CATACTAAAA CATCTTCAAC TCCTTGGGTC ACTACCTTGA TATAATCCCC

121 GCTGGTGTGG TTCTGGTACT GTACCAGGAA AACAGATTTC TAAAGGAAAT CAAATTAGGA
   CGACCACACC AAGACCATGA CATGGTCCTT TTGTCTAAAG ATTCCTTTA GTTTAATCCT

+1                               MetAsn IlePheLeu LeuAsnLeuLeu ThrGluGlu ValArgLeu
   ]-----

181 TAAGATTTGT ATCTGATGAA TATTTTCCTT CTGAACCTTC TAACAGAGGA GGTAAGATTA
   ATTCTAAACA TAGACTACTT ATAAAAGGAA GACTTGGAAG ATTGTCTCCT CCATTCTAAT

+1 TyrSerCysThr ProArgAsn PheSerVal SerIleArgGlu GluLeuLys ArgThrAsp
   -----

241 TACAGCTGCA CACCTCGTAA CTTCTCAGTG TCCATAAGGG AAGAACTAAA GAGAACCGAT
   ATGTCGACGT GTGGAGCATT GAAGAGTCAC AGGTATTCCC TTCTTGATTT CTCTTGGCTA

+1 ThrIlePheTrp ProGlyCys LeuLeuVal LysArgCysGly GlyAsnCys AlaCysCys
   -----

301 ACCATTTTCT GGCCAGGTTG TCTCCTGGTT AAACGCTGTG GTGGGAACTG TGCCTGTTGT
   TGGTAAAAGA CCGGTCCAAC AGAGGACCAA TTTGCGACAC CACCCTTGAC ACGGACAACA

+1 LeuHisAsnCys AsnGluCys GlnCysVal ProSerLysVal ThrLysLys TyrHisGlu
   -----

361 CTCCACAATT GCAATGAATG TCAATGTGTC CCAAGCAAAG TTAATAAAAA ATACCACGAG
   GAGGTGTTAA CGTTACTTAC AGTTACACAG GGTTCGTTTC AATGATTTTT TATGGTGCTC

+1 ValLeuGlnLeu ArgProLys ThrGlyVal ArgGlyLeuHis LysSerLeu ThrAspVal
   -----

421 GTCCTTCAGT TGAGACCAAA GACCGGTGTC AGGGGATTGC ACAAATCACT CACCGACGTG
   CAGGAAGTCA ACTCTGGTTT CTGGCCACAG TCCCCTAACG TGTTTAGTGA GTGGCTGCAC

+1 AlaLeuGluHis HisGluGlu CysAspCys ValCysArgGly SerThrGly Gly
   ----->

481 GCCCTGGAGC ACCATGAGGA GTGTGACTGT GTGTGCAGAG GGAGCACAGG AGGATAGCCG
   CGGGACCTCG TGGTACTCCT CACACTGACA CACACGTCTC CCTCGTGTCC TCCTATCGGC

541 CATCACCACC AGCAGCTCTT GCCCAGAGCT GTGCAGTGCA GTGGCTGATT CTATTAGAGA
   GTAGTGGTGG TCGTCGAGAA CGGGTCTCGA CACGTCACGT CACCGACTAA GATAATCTCT

601 ACGTATGCGT TATCTCCATC CTTAATCTCA GTTGTGTTGCT TCAAGGACCT TTCATCTTCA
   TGCATACGCA ATAGAGGTAG GAATTAGAGT CAACAAACGA AGTTCCTGGA AAGTAGAAGT
```

Fig. 1-1



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661	GGATTTACAG	TGCATTCTGA	AAGAGGAGAC	ATCAAACAGA	ATTAGGAGTT	GTGCAACAGC
	CCTAAATGTC	ACGTAAGACT	TTCTCCTCTG	TAGTTTGTCT	TAATCCTCAA	CACGTTGTCTG
721	TCTTTTGAGA	GGAGGCCTAA	AGGACAGGAG	AAAAGGTCTT	CAATCGTGGA	AAGAAAATTA
	AGAAAACTCT	CCTCCGGATT	TCCTGTCCTC	TTTTCCAGAA	GTTAGCACCT	TTCTTTTAAT
781	AATGTTGTAT	TAAATAGATC	ACCAGCTAGT	TTCAGAGTTA	CCATGTACGT	ATTCCACTAG
	TTACAACATA	ATTTATCTAG	TGGTCGATCA	AAGTCTCAAT	GGTACATGCA	TAAGGTGATC
841	CTGGGTTCTG	TATTTTCAGTT	CTTTCGATAC	GGCTTAGGGT	AATGTCAGTA	CAGGAAAAAA
	GACCCAAGAC	ATAAAGTCAA	GAAAGCTATG	CCGAATCCCA	TTACAGTCAT	GTCCTTTTTT
901	ACTGTGCAAG	TGAGCACCTG	ATTCCGTTGC	CTTGCTTAAC	TCTAAAGCTC	CATGTCCTGG
	TGACACGTTT	ACTCGTGGAC	TAAGGCAACG	GAACGAATTG	AGATTTCGAG	GTACAGGACC
961	GCCTAAAATC	GTATAAAATC	TGGATTTTTT	TTTTTTTTTT	TGCTCATATT	CACATATGTA
	CGGATTTTAG	CATATTTTAG	ACCTAAAAAA	AAAAAAAAAA	ACGAGTATAA	GTGTATACAT
1021	AACCAGAACA	TTCTATGTAC	TACAAACCTG	GTTTTTAAAA	AGGAACTATG	TTGCTATGAA
	TTGGTCTTGT	AAGATACATG	ATGTTTGGAC	CAAAAATTTT	TCCTTGATAC	AACGATACTT
1081	TTAAACTTGT	GTCGTGCTGA	TAGGACAGAC	TGGATTTTTT	ATATTTCTTA	TTAAAATTTT
	AATTTGAACA	CAGCACGACT	ATCCTGTCTG	ACCTAAAAAG	TATAAAGAAT	AATTTTAAAG
1141	TGCCATTTAG	AAGAAGAGAA	CTACATTCAT	GGTTTGGAAG	AGATAAACCT	GAAAAGAAGA
	ACGGTAAATC	TTCTTCTCTT	GATGTAAGTA	CCAAACCTTC	TCTATTTGGA	CTTTTCTTCT
1201	GTGGCCTTAT	CTTCACTTTA	TCGATAAGTC	AGTTTATTTG	TTTCATTGTG	TACATTTTTA
	CACCGGAATA	GAAGTGAAAT	AGCTATTTCAG	TCAAATAAAC	AAAGTAACAC	ATGTAAAAAT
1261	TATTCTCCTT	TTGACATTAT	AACTGTTGGC	TTTTCTAATC	TTGTAAATA	TATCTATTTT
	ATAAGAGGAA	AACTGTAATA	TTGACAACCG	AAAAGATTAG	AACAATTTAT	ATAGATAAAA
1321	TACCAAAGGT	ATTTAATATT	CTTTTTTATG	ACAACCTAGA	TCAACTATTT	TTAGCTTGGT
	ATGGTTTCCA	TAAATTATAA	GAAAAAATAC	TGTTGAATCT	AGTTGATAAA	AATCGAACCA
1381	AAATTTTCT	AAACACAATT	GTTATAGCCA	GAGGAACAAA	GATGATATAA	AATATTGTTG
	TTTAAAAAGA	TTTGTGTTAA	CAATATCGGT	CTCCTTGTTT	CTACTATATT	TTATAACAAC
1441	CTCTGACAAA	AATACATGTA	TTTCATTCTC	GTATGGTGCT	AGAGTTAGAT	TAATCTGCAT
	GAGACTGTTT	TTATGTACAT	AAAGTAAGAG	CATACCACGA	TCTCAATCTA	ATTAGACGTA
1501	TTTAAAAAAC	TGAATTGGAA	TAGAATTGGT	AAGTTGCAAA	GACTTTTTGA	AAATAATTAA
	AAATTTTGTG	ACTTAACCTT	ATCTTAACCA	TTCAACGTTT	CTGAAAAACT	TTTATTAATT

Fig. 1-2



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1561 ATTATCATAT CTTCCATTCC TGTTATTGGA GATGAAAATA AAAAGCAACT TATGAAAGTA  
TAATAGTATA GAAGGTAAGG ACAATAACCT CTACTTTTAT TTTTCGTTGA ATACTTTCAT

1621 GACATTCAGA TCCAGCCATT ACTAACCTAT TCCTTTTTTG GGGAAATCTG AGCCTAGCTC  
CTGTAAAGTCT AGGTCGGTAA TGATTGGATA AGGAAAAAAC CCCTTTAGAC TCGGATCGAG

1681 AGAAAAACAT AAAGCACCTT GAAAAAGACT TGGCAGCTTC CTGATAAAGC GTGCTGTGCT  
TCTTTTTGTA TTTCGTGGAA CTTTTTCTGA ACCGTCGAAG GACTATTTCTG CACGACACGA

1741 GTGCAGTAGG AACACATCCT ATTTATTGTG ATGTTGTGGT TTTATTATCT TAAACTCTGT  
CACGTCATCC TTGTGTAGGA TAAATAACAC TACAACACCA AAATAATAGA ATTTGAGACA

1801 TCCATACACT TGTATAAATA CATGGATATT TTTATGTACA GAAGTATGTC TCTTAACCAG  
AGGTATGTGA ACATATTTAT GTACCTATAA AAATACATGT CTTCATAACAG AGAATTGGTC

1861 TTCACTTATT GTACCTGG  
AAGTGAATAA CATGGACC

Fig. 1-3



VASCULAR ENDOTHELIAL GROWTH  
FACTOR-X  
Robert D. Gordon, et al.  
Serial No.: 09/468,647

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PREDICTED VEGF-LIKE PROTEIN ENCODED BY INCYTE CONTIG OF 8/12/98

```
1  MNIFLLNLLT  EEVRLYSCTP  RNFSVSIREE  LKRTDTIFWP  GCLLVKRCGG
51  NCACCLHNCN  ECQCVPSKVT  KKYHEVLQLR  PKTGVRGLHK  SLTDVALEHH
101 EECDVCVRGS  TGG
```

Fig. 2



PCR PRIMERS FOR CLONING VEGF-X

vegfx1 AAAATGTATGGATACTTAC

vegfx2 GTTTGATGAAAGATTGGCTTG

vegfx3 TTTCTAAAGGAAATCAAATTAG

vegfx4 GATAAGATTGTATCTGATG

vegfx5 GATGTCTCCTCTTTCAG

vegfx6 GCACAACTCCTAATTCTG

vegfx7 AGCACCTGATTCCGTTGC

vegfx8 TAGTACATAGAATGTTCTGG

vegfx9 AAGAGACATACTTCTGTAC

vegfx10 CCAGGTACAATAAGTGAAGTGA

Fig. 3





VASCULAR ENDOTHELIAL GROWTH  
FACTOR-X  
Robert D. Gordon, et al.  
Serial No.: 09/468,647

7/66

VEGF-X 5' RACE PRIMERS

vegfx11 CCTTTAGAAATCTGTTTTCTGGTACAG

vegfx12 GGAAAATATTCATCAGATACAAATCTTATCC

vegfx13 GGTCCAGTGGCAAAGCTGAAGG

vegfx14 CTGGTTCAAGATATCGAATAAGGTCTTCC

Fig. 5



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DNA SEQUENCE ASSEMBLED FROM IN-HOUSE CLONES AND 5'RACE

```
1  TGCCAGAGCA GGTGGGCGCT TCCACCCAG TGCAGCCTTC CCCTGGCGGT GGTGAAAGAG
   ACGGTCTCGT CCACCCGCGA AGGTGGGGTC ACGTCGGAAG GGGACCGCCA CCACTTTCTC

61  ACTCGGGAGT CGCTGCTTCC AAAGTGCCCG CCGTGAGTGA GCTCTCACCC CAGTCAGCCA
   TGAGCCCTCA GCGACGAAGG TTTCACGGGC GGCACCTACT CGAGAGTGGG GTCAGTCGGT

+2  MetSerLeu PheGlyLeuLeu LeuLeuThr SerAlaLeu AlaGlyGlnArg GlnGlyTh
   ]-----
121  AATGAGCCTC TTCGGGCTTC TCCTGCTGAC ATCTGCCCTG GCCGGCCAGA GACAGGGGAC
   TTACTCGGAG AAGCCCGAAG AGGACGACTG TAGACGGGAC CGGCCGGTCT CTGTCCCCTG

+2  rGlnAlaGlu SerAsnLeuSer SerLysPhe GlnPheSer SerAsnLysGlu GlnAsnGl
   -----
181  TCAGGCGGAA TCCAACCTGA GTAGTAAATT CCAGTTTTTC AGCAACAAGG AACAGAACGG
   AGTCCGCCTT AGGTTGGACT CATCATTTAA GGTCAAAAGG TCGTTGTTCC TTGTCTTGCC

+2  yValGlnAsp ProGlnHisGlu ArgIleIle ThrValSer ThrAsnGlySer IleHisSe
   -----
241  AGTACAAGAT CCTCAGCATG AGAGAATTAT TACTGTGTCT ACTAATGGAA GTATTCACAG
   TCATGTTCTA GGAGTCGTAC TCTCTTAATA ATGACACAGA TGATTACCTT CATAAGTGTC

+2  rProArgPhe ProHisThrTyr ProArgAsn ThrValLeu ValTrpArgLeu ValAlaVa
   -----
301  CCCAAGGTTT CCTCATACTT ATCCAAGAAA TACGGTCTTG GTATGGAGAT TAGTAGCAGT
   GGGTTCCAAA GGAGTATGAA TAGGTTCTTT ATGCCAGAAC CATACTCTA ATCATCGTCA

+2  lGluGluAsn ValTrpIleGln LeuThrPhe AspGluArg PheGlyLeuGlu AspProGl
   -----
361  AGAGGAAAAT GTATGGATAC AACTTACGTT TGATGAAAGA TTTGGGCTTG AAGACCCAGA
   TCTCCTTTTA CATACCTATG TTGAATGCAA ACTACTTTCT AAACCCGAAC TTCTGGGTCT

+2  uAspAspIle CysLysTyrAsp PheValGlu ValGluGlu ProSerAspGly ThrIleLe
   -----
421  AGATGACATA TGCAAGTATG ATTTTGTAGA AGTTGAGGAA CCCAGTGATG GAACTATATT
   TCTACTGTAT ACGTTCATAC TAAAACATCT TCAACTCCTT GGGTCACTAC CTTGATATAA

+2  uGlyArgTrp CysGlySerGly ThrValPro GlyLysGln IleSerLysGly AsnGlnIl
   -----
481  AGGGCGCTGG TGTGGTCTG GTACTGTACC AGGAAAACAG ATTTCTAAAG GAAATCAAAT
   TCCCGCGACC ACACCAAGAC CATGACATGG TCCTTTTGTC TAAAGATTTT CTTTAGTTTA

+2  eArgIleArg PheValSerAsp GluTyrPhe ProSerGlu ProGlyPheCys IleHisTy
   -----
541  TAGGATAAGA TTTGTATCTG ATGAATATTT TCCTTCTGAA CCAGGGTTCT GCATCCACTA
   ATCCTATTCT AAACATAGAC TACTTATAAA AGGAAGACTT GGTCCCAAGA CGTAGGTGAT
```

Fig. 6-1





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```
+2 rAsnIleVal MetProGlnPhe ThrGluAla ValSerPro SerValLeuPro ProSerAl
-----
601 CAACATTGTC ATGCCACAAT TCACAGAAGC TGTGAGTCCT TCAGTGCTAC CCCCTTCAGC
    GTTGTAAACAG TACGGTGTTA AGTGTCTTCG AACTCAGGA AGTCACGATG GGGGAAGTCG

+2 aLeuProLeu AspLeuLeuAsn AsnAlaIle ThrAlaPhe SerThrLeuGlu AspLeuIl
-----
661 TTTGCCACTG GACCTGCTTA ATAATGCTAT AACTGCCTTT AGTACCTTGG AAGACCTTAT
    AAACGGTGAC CTGGACGAAT TATTACGATA TTGACGGAAA TCATGGAACC TTCTGGAATA

+2 eArgTyrLeu GluProGluArg TrpGlnLeu AspLeuGlu AspLeuTyrArg ProThrTr
-----
721 TCGATATCTT GAACCAGAGA GATGGCAGTT GGACTTAGAA GATCTATATA GGCCAACTTG
    AGCTATAGAA CTTGGTCTCT CTACCGTCAA CCTGAATCTT CTAGATATAT CCGGTTGAAC

+2 pGlnLeuLeu GlyLysAlaPhe ValPheGly ArgLysSer ArgValValAsp LeuAsnLe
-----
781 GCAACTTCTT GGCAAGGCTT TTGTTTTTGG AAGAAAATCC AGAGTGGTGG ATCTGAACCT
    CGTTGAAGAA CCGTTCGGAA AACAAAAACC TTCTTTTAGG TCTCACCACC TAGACTTGGA

+2 uLeuThrGlu GluValArgLeu TyrSerCys ThrProArg AsnPheSerVal SerIleAr
-----
841 TCTAACAGAG GAGGTAAGAT TATACAGCTG CACACCTCGT AACTTCTCAG TGTCCATAAG
    AGATTGTCTC CTCCATTCTA ATATGTCGAC GTGTGGAGCA TTGAAGAGTC ACAGGTATTC

+2 gGluGluLeu LysArgThrAsp ThrIlePhe TrpProGly CysLeuLeuVal LysArgCy
-----
901 GGAAGAACTA AAGAGAACCG ATACCATTTT CTGGCCAGGT TGTCTCCTGG TTAAACGCTG
    CCTTCTTGAT TTCTCTTGGC TATGGTAAAA GACCGGTCCA ACAGAGGACC AATTTGCGAC

+2 sGlyGlyAsn CysAlaCysCys LeuHisAsn CysAsnGlu CysGlnCysVal ProSerLy
-----
961 TGGTGGGAAC TGTGCCTGTT GTCTCCACAA TTGCAATGAA TGTCAATGTG TCCAAGCAA
    ACCACCCTTG ACACGGACAA CAGAGGTGTT AACGTTACTT ACAGTTACAC AGGGTTCGTT

+2 sValThrLys LysTyrHisGlu ValLeuGln LeuArgPro LysThrGlyVal ArgGlyLe
-----
1021 AGTTACTAAA AAATACCACG AGGTCCTTCA GTTGAGACCA AAGACCGGTG TCAGGGGATT
    TCAATGATTT TTTATGGTGC TCCAGGAAGT CAACTCTGGT TTCTGGCCAC AGTCCCCTAA

+2 uHisLysSer LeuThrAspVal AlaLeuGlu HisHisGlu GluCysAspCys ValCysAr
-----
1081 GCACAAATCA CTCACCGACG TGGCCCTGGA GCACCATGAG GAGTGTGACT GTGTGTGCAG
    CGTGTTTAGT GAGTGGCTGC ACCGGGACCT CGTGGTACTC CTCACACTGA CACACACGTC
```

Fig. 6-2



10/66

+2 gGlySerThr GlyGly  
----->

1141	AGGGAGCACA	GGAGGATAGC	CGCATCACCA	CCAGCAGCTC	TTGCCCAGAG	CTGTGCAGTG
	TCCCTCGTGT	CCTCCTATCG	GCGTAGTGGT	GGTCGTCGAG	AACGGGTCTC	GACACGTCAC
1201	CAGTGGCTGA	TTCTATTAGA	GAACGTATGC	GTTATCTCCA	TCCTTAATCT	CAGTTGTTTG
	GTCACCGACT	AAGATAATCT	CTTGCATACG	CAATAGAGGT	AGGAATTAGA	GTCAACAAAC
1261	CTTCAAGGAC	CTTTCATCTT	CAGGATTTAC	AGTGCATTCT	GAAAGAGGAG	ACATCAAACA
	GAAGTTCCTG	GAAAGTAGAA	GTCCTAAATG	TCACGTAAGA	CTTTCTCCTC	TGTAGTTTGT
1321	GAATTAGGAG	TTGTGCAACA	GCTCTTTTGA	GAGGAGGCCT	AAAGGACAGG	AGAAAAGGTC
	CTTAATCCTC	AACACGTTGT	CGAGAAAAC	CTCCTCCGGA	TTTCTGTCC	TCTTTTCCAG
1381	TTCAATCGTG	GAAAGAAAAT	TAAATGTTGT	ATTAAATAGA	TCACCAGCTA	GTTTCAGAGT
	AAGTTAGCAC	CTTCTTTTAA	ATTTACAACA	TAATTTATCT	AGTGGTCGAT	CAAAGTCTCA
1441	TACCATGTAC	GTATTCCACT	AGCTGGGTTC	TGTATTTTCA	TTCTTTTCGAT	ACGGCTTAGG
	ATGGTACATG	CATAAGGTGA	TCGACCCAAG	ACATAAAGTC	AAGAAAGCTA	TGCCGAATCC
1501	GTAATGTCAG	TACAGGAAAA	AAACTGTGCA	AGTGAGCACC	TGATTCCGTT	GCCTTGCTTA
	CATTACAGTC	ATGTCCTTTT	TTTGACACGT	TCACTCGTGG	ACTAAGGCAA	CGGAACGAAT
1561	ACTCTAAAGC	TCCATGTCCT	GGGCCTAAAA	TCGTATAAAA	TCTGGATTTT	TTTTTTTTTT
	TGAGATTTTC	AGGTACAGGA	CCCGGATTTT	AGCATATTTT	AGACCTAAAA	AAAAAAAAAA
1621	TTTGCTCATA	TTACATATG	TAAACCAGAA	CATTCTATGT	ACTACAAACC	TGGTTTTTAA
	AAACGAGTAT	AAGTGTATAC	ATTTGGTCTT	GTAAGATACA	TGATGTTTGG	ACCAAAAATT
1681	AAAGGAACTA	TGTTGCTATG	AATTAACTT	GTGTCGTGCT	GATAGGACAG	ACTGGATTTT
	TTTCCTTGAT	ACAACGATAC	TTAATTTGAA	CACAGCACGA	CTATCCTGTC	TGACCTAAAA
1741	TCATATTTCT	TATTAAAATT	TCTGCCATTT	AGAAGAAGAG	AACTACATTC	ATGGTTTGGA
	AGTATAAAGA	ATAATTTTAA	AGACGGTAAA	TCTTCTTCTC	TTGATGTAAG	TACCAAACCT
1801	AGAGATAAAC	CTGAAAAGAA	GAGTGGCCTT	ATCTTCACTT	TATCGATAAG	CCAGTTTATT
	TCTCTATTTG	GACTTTTCTT	CTCACCAGAA	TAGAAGTGAA	ATAGCTATTC	GGTCAAATAA
1861	TGTTTCATTG	TGTACATTTT	TATATTCTCC	TTTTGACATT	ATAACTGTTG	GCTTTTCTAA
	ACAAAGTAAC	ACATGTAAAA	ATATAAGAGG	AAAACGTGAA	TATTGACAAC	CGAAAAGATT
1921	TCTTGTTAAA	TATATCTATT	TTTACCAAAG	GTATTTAATA	TTCTTTTTTA	TGACAACTTA
	AGAACAATTT	ATATAGATAA	AAATGGTTTC	CATAAATTAT	AAGAAAAAAT	ACTGTTGAAT

Fig. 6-3



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1981 GATCAACTAT TTTTAGCTTG GTAAATTTTT CTAAACACAA TTGTTATAGC CAGAGGAACA  
CTAGTTGATA AAAATCGAAC CATTTAAAAA GATTGTGTGTT AACAAATATCG GTCTCCTTGT

2041 AAGATGATAT AAAATATTGT TGCTCTGACA AAAATACATG TATTTTCATTC TCGTATGGTG  
TTCTACTATA TTTTATAACA ACGAGACTGT TTTTATGTAC ATAAAGTAAG AGCATAACCAC

2101 CTAGAGTTAG ATTAATCTGC ATTTTAAAAA ACTGAATTGG AATAGAATTG GTAAGTTGCA  
GATCTCAATC TAATTAGACG TAAAATTTTT TGACTTAACC TTATCTTAAC CATTCAACGT

2161 AAGACTTTTT GAAAATAATT AAATTATCAT ATCTTCCATT CCTGTTATTG GAGATGAAAA  
TTCTGAAAAA CTTTTATTAA TTTAATAGTA TAGAAGGTAA GGACAATAAC CTCTACTTTT

2221 TAAAAAGCAA CTTATGAAAG TAGACATTCA GATCCAGCCA TTAATAACCT ATTCCTTTTT  
ATTTTTTCGTT GAATACTTTC ATCTGTAAGT CTAGGTCGGT AATGATTGGA TAAGGAAAAA

2281 TGGGGAAATC TGAGCCTAGC TCAGAAAAAC ATAAAGCACC TTGAAAAAGA CTTGGCAGCT  
ACCCCTTTAG ACTCGGATCG AGTCTTTTTG TATTTTCGTGG AACTTTTTTCT GAACCGTCGA

2341 TCCTGATAAA GCGTGCTGTG CTGTGCAGTA GGAACACATC CTATTTATTG TGATGTTGTG  
AGGACTATTT CGCACGACAC GACACGTCAT CCTTGTGTAG GATAAATAAC ACTACAACAC

2401 GTTTTATTAT CTTAAACTCT GTTCCATACA CTTGTATAAA TACATGGATA TTTTATGTA  
CAAAATAATA GAATTTGAGA CAAGGTATGT GAACATATTT ATGTACCTAT AAAAATACAT

2461 CAGAAGTATG TCTCT  
GTCTTCATAC AGAGA

Fig. 6-4



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NEW SEQUENCE + INCYTE ESTS

```
1  ATTTGTTTAA ACCTTGGGAA ACTGGTTCAG GTCCAGGTTT TGCTTTGATC CTTTTCAAAA
   TAAACAAATT TGGAACCCTT TGACCAAGTC CAGGTCCAAA ACGAAACTAG GAAAAGTTTT

61  ACTGGAGACA CAGAAGAGGG CTTCTAGGAA AAAGTTTTTG GATGGGATTA TGTGGAAACT
   TGACCTCTGT GTCTTCTCCC GAAGATCCTT TTTCAAAACC CTACCCTAAT ACACCTTTGA

121 ACCCTGCGAT TCTCTGCTGC CAGAGCAGGC TCGGCGCTTC CACCCAGTG CAGCCTTCCC
   TGGGACGCTA AGAGACGACG GTCTCGTCCG AGCCGCGAAG GTGGGGTCAC GTCGGAAGGG

181 CTGGCGGTGG TGAAAGAGAC TCGGGAGTCG CTGCTTCCAA AGTGCCCGCC GTGAGTGAGC
   GACCGCCACC ACTTTCTCTG AGCCCTCAGC GACGAAGGTT TCACGGGCGG CACTCACTCG

+2                               Met SerLeuPhe GlyLeuLeu LeuLeuThrSer AlaLeuAl
   ]-----

241 TCTCACCCCA GTCAGCCAAA TGAGCCTCTT CGGGCTTCTC CTGCTGACAT CTGCCCTGGC
   AGAGTGGGGT CAGTCGGTTT ACTCGGAGAA GCCCGAAGAG GACGACTGTA GACGGGACCG

+2 aGlyGlnArg GlnGlyThrGln AlaGluSer AsnLeuSer SerLysPheGln PheSerSe
   -----

301 CGGCCAGAGA CAGGGGACTC AGGCGGAATC CAACCTGAGT AGTAAATTCC AGTTTTCCAG
   GCCGGTCTCT GTCCCTGAG TCCGCCTTAG GTTGGACTCA TCATTTAAGG TCAAAGGTC

+2 rAsnLysGlu GlnTyrGlyVal GlnAspPro GlnHisGlu ArgIleIleThr ValSerTh
   -----

361 CAACAAGGAA CAGTACGGAG TACAAGATCC TCAGCATGAG AGAATTATTA CTGTGTCTAC
   GTTGTTCCTT GTCATGCCTC ATGTTCTAGG AGTCGTA CTCTTAATAAT GACACAGATG

+2 rAsnGlySer IleHisSerPro ArgPhePro HisThrTyr ProArgAsnThr ValLeuVa
   -----

421 TAATGGAAGT ATTCACAGCC CAAGGTTTCC TCATACTTAT CCAAGAAATA CGGTCTTGGT
   ATTACCTTCA TAAGTGTCGG GTTCCAAAGG AGTATGAATA GGTTCTTTAT GCCAGAACCA

+2 lTrpArgLeu ValAlaValGlu GluAsnVal TrpIleGln LeuThrPheAsp GluArgPh
   -----

481 ATGGAGATTA GTAGCAGTAG AGGAAAATGT ATGGATACAA CTTACGTTTG ATGAAAGATT
   TACCTCTAAT CATCGTCATC TCCTTTTACA TACCTATGTT GAATGCAAAC TACTTTCTAA
```

Fig. 7-1



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```
+2 eGlyLeuGlu AspProGluAsp AspIleCys LysTyrAsp PheValGluVal GluGluPr
-----
541 TGGGCTTGAA GACCCAGAAG ATGACATATG CAAGTATGAT TTTGTAGAAG TTGAGGAACC
    ACCCGAAGCTT CTGGGTCTTC TACTGTATAC GTTCATACTA AAACATCTTC AACTCCTTGG

+2 oSerAspGly ThrIleLeuGly ArgTrpCys GlySerGly ThrValProGly LysGlnIl
-----
601 CAGTGATGGA ACTATATTAG GCGCTGGTG TGGTCTGGT ACTGTACCAG GAAAACAGAT
    GTCCTACCT TGATATAATC CCGCGACCAC ACCAAGACCA TGACATGGTC CTTTGTCTA

+2 eSerLysGly AsnGlnIleArg IleArgPhe ValSerAsp GluTyrPhePro SerGluPr
-----
661 TTCTAAAGGA AATCAAATTA GGATAAGATT TGTATCTGAT GAATATTTTC CTTCTGAACC
    AAGATTTCTT TTAGTTTAAT CCTATTCTAA ACATAGACTA CTTATAAAAG GAAGACTTGG

+2 oGlyPheCys IleHisTyrAsn IleValMet ProGlnPhe ThrGluAlaVal SerProSe
-----
721 AGGGTTCTGC ATCCACTACA ACATTGTCAT GCCACAATTC ACAGAAGCTG TGAGTCCTTC
    TCCCAAGACG TAGGTGATGT TGTAACAGTA CGGTGTAAAG TGTCTTCGAC ACTCAGGAAG

+2 rValLeuPro ProSerAlaLeu ProLeuAsp LeuLeuAsn AsnAlaIleThr AlaPheSe
-----
781 AGTGCTACCC CCTTCAGCTT TGCCACTGGA CTGCTTAAT AATGCTATAA CTGCCTTTAG
    TCACGATGGG GGAAGTCGAA ACGGTGACCT GGACGAATTA TTACGATATT GACGGAAATC

+2 rThrLeuGlu AspLeuIleArg TyrLeuGlu ProGluArg TrpGlnLeuAsp LeuGluAs
-----
841 TACCTTGGA GACCTTATTC GATATCTTGA ACCAGAGAGA TGGCAGTTGG ACTTAGAAGA
    ATGGAACCTT CTGGAATAAG CTATAGAACT TGGTCTCTCT ACCGTCAACC TGAATCTTCT

+2 pLeuTyrArg ProThrTrpGln LeuLeuGly LysAlaPhe ValPheGlyArg LysSerAr
-----
901 TCTATATAGG CCAACTTGGC AACTTCTTGG CAAGGCTTTT GTTTTGGAA GAAAATCCAG
    AGATATATCC GGTGGAACCG TTGAAGAACC GTTCCGAAAA CAAAACCTT CTTTLAGGTC

+2 gValValAsp LeuAsnLeuLeu ThrGluGlu ValArgLeu TyrSerCysThr ProArgAs
-----
961 AGTGGTGGAT CTGAACCTTC TAACAGAGGA GGTAAGATTA TACAGCTGCA CACCTCGTAA
    TCACCACCTA GACTTGGAAG ATTGTCTCCT CCATTCTAAT ATGTCGACGT GTGGAGCATT

+2 nPheSerVal SerIleArgGlu GluLeuLys ArgThrAsp ThrIlePheTrp ProGlyCy
-----
1021 CTTCTCAGTG TCCATAAGGG AAGAACTAAA GAGAACCGAT ACCATTTTCT GGCCAGGTTG
    GAAGAGTCAC AGGTATTCCC TTCTTGATTT CTCTTGGCTA TGGTAAAAGA CCGGTCCAAC
```

Fig. 7-2



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```
+2 sLeuLeuVal LysArgCysGly GlyAsnCys AlaCysCys LeuHisAsnCys AsnGluCy
-----
1081 TCTCCTGGTT AAACGCTGTG GTGGGAAGTGT TGCCTGTTGT CTCCACAATT GCAATGAATG
AGAGGACCAA TTTGCGACAC CACCCTTGAC ACGGACAACA GAGGTGTTAA CGTTACTTAC

+2 sGlnCysVal ProSerLysVal ThrLysLys TyrHisGlu ValLeuGlnLeu ArgProLy
-----
1141 TCAATGTGTC CCAAGCAAAG TTAATAAAAA ATACCACGAG GTCCTTCAGT TGAGACCAAA
AGTTACACAG GGTTCGTTTC AATGATTTTT TATGGTGCTC CAGGAAGTCA ACTCTGGTTT

+2 sThrGlyVal ArgGlyLeuHis LysSerLeu ThrAspVal AlaLeuGluHis HisGluGl
-----
1201 GACCGGTGTC AGGGGATTGC ACAAATCACT CACCGACGTG GCCCTGGAGC ACCATGAGGA
CTGGCCACAG TCCCCTAACG TGTTTAGTGA GTGGCTGCAC CGGGACCTCG TGGTACTCCT

+2 uCysAspCys ValCysArgGly SerThrGly Gly
----->
1261 GTGTGACTGT GTGTGCAGAG GGAGCACAGG AGGATAGCCG CATCACCACC AGCAGCTCTT
CACACTGACA CACACGTCTC CCTCGTGTCC TCCTATCGGC GTAGTGGTGG TCGTCGAGAA

1321 GCCCAGAGCT GTGCAGTGCA GTGGCTGATT CTATTAGAGA ACGTATGCGT TATCTCCATC
CGGGTCTCGA CACGTCACGT CACCGACTAA GATAATCTCT TGCATACGCA ATAGAGGTAG

1381 CTTAATCTCA GTTGTGTTGCT TCAAGGACCT TTCATCTTCA GGATTTACAG TGCATTCTGA
GAATTAGAGT CAACAAACGA AGTTCCTGGA AAGTAGAAGT CCTAAATGTC ACGTAAGACT

1441 AAGAGGAGAC ATCAAACAGA ATTAGGAGTT GTGCAACAGC TCTTTTGAGA GGAGGCCTAA
TTCTCCTCTG TAGTTTGTCT TAATCCTCAA CACGTTGTCT AGAAAACTCT CCTCCGGATT

1501 AGGACAGGAG AAAAGGTCTT CAATCGTGGA AAGAAAATTA AATGTTGTAT TAAATAGATC
TCCTGTCTCT TTTTCCAGAA GTTAGCACCT TTCTTTTAAT TTACAACATA ATTTATCTAG

1561 ACCAGCTAGT TTCAGAGTTA CCATGTACGT ATTCCACTAG CTGGGTTCTG TATTTTCAGTT
TGGTCGATCA AAGTCTCAAT GGTACATGCA TAAGGTGATC GACCCAAGAC ATAAAGTCAA

1621 CTTTCGATAC GGCTTAGGGT AATGTCAGTA CAGGAAAAAA ACTGTGCAAG TGAGCACCTG
GAAAGCTATG CCGAATCCCA TTACAGTCAT GTCCTTTTTT TGACACGTTT ACTCGTGGAC

1681 ATTCCGTTGC CTTGGCTTAA CTCTAAAGCT CCATGTCCTG GGCCTAAAAT CGTATAAAAT
TAAGGCAACG GAACCGAATT GAGATTTCTG GGTACAGGAC CCGGATTTTA GCATATTTTA

1741 CTGGATTTTT TTTTTTTTTT TTGCGCATAT TCACATATGT AAACCAGAAC ATTCTATGTA
GACCTAAAAA AAAAAAAAAA AACGCGTATA AGTGATATACA TTTGGTCTTG TAAGATACAT

1801 CTACAAACCT GGTTTTTAAA AAGGAACAT GTTGCTATGA ATTAACTTG TGTCATGCTG
GATGTTTGA CCAAAAATTT TTCCTTGATA CAACGATACT TAATTTGAAC ACAGTACGAC
```

Fig. 7-3



VASCULAR ENDOTHELIAL GROWTH  
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1861	ATAGGACAGA	CTGGATTTTT	CATATTCTT	ATTAAAATT	CTGCCATTTA	GAAGAAGAGA
	TATCCTGTCT	GACCTAAAAA	GTATAAAGAA	TAATTTTAAA	GACGGTAAAT	CTTCTTCTCT
1921	ACTACATTCA	TGGTTTGGAA	GAGATAAACC	TGAAAAGAAG	AGTGGCCTTA	TCTTCACTTT
	TGATGTAAGT	ACCAAACCTT	CTCTATTTGG	ACTTTTCTTC	TCACCGGAAT	AGAAGTGAAA
1981	ATCGATAAGT	CAGTTTATTT	GTTTCATTGT	GTACATTTTT	ATATTCTCCT	TTTGACATTA
	TAGCTATTCA	GTCAAATAAA	CAAAGTAACA	CATGTAAAAA	TATAAGAGGA	AAACTGTAAT
2041	TAACTGTTGG	CTTTTCTAAT	CTTGTTAAAT	ATATCTATTT	TTACCAAAGG	TATTTAATAT
	ATTGACAACC	GAAAAGATTA	GAACAATTTA	TATAGATAAA	AATGGTTTCC	ATAAATTATA
2101	TCTTTTTTAT	GACAACTTAG	ATCAACTATT	TTTAGCTTGG	TAAATTTTTT	TAAACACAAT
	AGAAAAATA	CTGTTGAATC	TAGTTGATAA	AAATCGAACC	ATTTAAAAAG	ATTTGTGTTA
2161	TGTTATAGCC	AGAGGAACAA	AGATGATATA	AAATATTGTT	GCTCTGACAA	AAATACATGT
	ACAATATCGG	TCTCCTTGTT	TCTACTATAT	TTTATAACAA	CGAGACTGTT	TTTATGTACA
2221	ATTCATTCT	CGTATGGTGC	TAGAGTTAGA	TTAATCTGCA	TTTTAAAAAA	CTGAATTGGA
	TAAAGTAAGA	GCATACCACG	ATCTCAATCT	AATTAGACGT	AAAATTTTTT	GACTTAACCT
2281	ATAGAATTGG	TAAGTTGCAA	AGACTTTTTG	AAAATAATTA	AATTATCATA	TCTTCCATTC
	TATCTTAACC	ATTCAACGTT	TCTGAAAAAC	TTTTATTAAT	TTAATAGTAT	AGAAGGTAAG
2341	CTGTTATTGG	AGATGAAAAAT	AAAAAGCAAC	TTATGAAAAGT	AGACATTGAG	ATCCAGCCAT
	GACAATAACC	TCTACTTTTA	TTTTTCGTTG	AATACTTTCA	TCTGTAAGTC	TAGGTCGGTA
2401	TACTAACCTA	TTCCTTTTTT	GGGGAAATCT	GAGCCTAGCT	CAGAAAAACA	TAAAGCACCT
	ATGATTGGAT	AAGGAAAAAA	CCCCTTTAGA	CTCGGATCGA	GTCTTTTTGT	ATTTTCGTGA
2461	TGAAAAAGAC	TTGGCAGCTT	CCTGATAAAG	CGTGCTGTGC	TGTGCAGTAG	GAACACATCC
	ACTTTTTCTG	AACCGTCGAA	GGACTATTTT	GCACGACACG	ACACGTCATC	CTTGTGTAGG
2521	TATTTATTGT	GATGTTGTGG	TTTTATTATC	TTAAACTCTG	TTCCATACAC	TTGTATAAAT
	ATAAATAACA	CTACAACACC	AAAATAATAG	AATTTGAGAC	AAGGTATGTG	AACATATTTA
2581	ACATGGATAT	TTTTATGTAC	AGAAGTATGT	CTCTTAACCA	GTTCACTTAT	TGTACTCTGG
	TGTACCTATA	AAAATACATG	TCTTCATACA	GAGAATTGGT	CAAGTGAATA	ACATGAGACC
2641	CAATTTAAAA	GAAAATCAGT	AAAATATTTT	GCTTGTAATA	TGCTTAATAT	CGTGCCTAGG
	GTTAAATTTT	CTTTTAGTCA	TTTTATAAAA	CGAACATTTT	ACGAATTATA	GCACGGATCC
2701	TTATGTGGTG	ACTATTTGAA	TCAAAAATGT	ATTGAATCAT	CAAATAAAAG	AATGTGGCTA
	AATACACCAC	TGATAAACTT	AGTTTTTACA	TAACCTAGTA	GTTTATTTTC	TTACACCGAT
2761	TTTTGGGGAG	AAAATT				
	AAAACCCCTC	TTTTAA				

Fig. 7-4



VASCULAR ENDOTHELIAL GROWTH  
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ADDITIONAL OLIGONUCLEOTIDES USED FOR AMPLIFICATION  
OF ENTIRE CODING REGION

5' - 1    TTTGTTTAAACCTTGGGAAACTGG

5' - 2    GTCCAGGTTTTGCTTTGATCC

Fig. 8





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DNA SEQUENCE OF CLONES 4 & 7, IDENTICAL CLONES CONTAINING THE  
ENTIRE OPEN READING FRAME

```
1  TTTGTTTAAA CCTTGGGAAA CTGGTTCAGG TCCAGGTTTT GCTTTGATCC TTTTCAAAAA
   AAACAAATTT GGAACCCTTT GACCAAGTCC AGGTCCAAAA CGAAACTAGG AAAAGTTTTT

61  CTGGAGACAC AGAAGAGGGC TCTAGGAAAA AGTTTTGGAT GGGATTATGT GGAAACTACC
   GACCTCTGTG TCTTCTCCCG AGATCCTTTT TCAAAACCTA CCCTAATACA CTTTGATGG

121 CTGCGATTCT CTGCTGCCAG AGCAGGCTCG GCGCTTCCAC CCCAGTGCAG CTTTCCCCTG
   GACGCTAAGA GACGACGGTC TCGTCCGAGC CGCGAAGGTG GGGTCACGTC GGAAGGGGAC

181 GCGGTGGTGA AAGAGACTCG GGAGTCGCTG CTTCCAAAGT GCCCGCCGTG AGTGAGCTCT
   CGCCACCACT TTCTCTGAGC CCTCAGCGAC GAAGGTTTCA CGGGCGGCAC TCACTCGAGA

+2                               MetSer LeuPheGly LeuLeuLeu LeuThrSerAla LeuAlaGl
   ]-----

241 CACCCAGTC AGCCAAATGA GCCTCTTCGG GCTTCTCCTG CTGACATCTG CCCTGGCCGG
   GTGGGGTCAG TCGGTTTACT CGGAGAAAGCC CGAAGAGGAC GACTGTAGAC GGGACCGGCC

+2 yGlnArgGln GlyThrGlnAla GluSerAsn LeuSerSer LysPheGlnPhe SerSerAs
   -----

301 CCAGAGACAG GGGACTCAGG CGGAATCCAA CCTGAGTAGT AAATTCCAGT TTTCCAGCAA
   GGTCTCTGTC CCCTGAGTCC GCCTTAGGTT GGACTCATCA TTTAAGGTCA AAAGGTCGTT

+2 nLysGluGln AsnGlyValGln AspProGln HisGluArg IleIleThrVal SerThrAs
   -----

361 CAAGGAACAG AACGGAGTAC AAGATCCTCA GCATGAGAGA ATTATTACTG TGTCTACTAA
   GTTCCTTGTC TTGCCTCATG TTCTAGGAGT CGTACTCTCT TAATAATGAC ACAGATGATT

+2 nGlySerIle HisSerProArg PheProHis ThrTyrPro ArgAsnThrVal LeuValTr
   -----

421 TGGAAGTATT CACAGCCCAA GGTTTCCTCA TACTTATCCA AGAAATACGG TCTTGGTATG
   ACCTTCATAA GTGTCGGGTT CCAAAGGAGT ATGAATAGGT TCTTTATGCC AGAACCATAC

+2 pArgLeuVal AlaValGluGlu AsnValTrp IleGlnLeu ThrPheAspGlu ArgPheGl
   -----

481 GAGATTAGTA GCAGTAGAGG AAAATGTATG GATACAACTT ACGTTTGATG AAAGATTTGG
   CTCTAATCAT CGTCATCTCC TTTTACATAC CTATGTTGAA TGCAAACCTAC TTTCTAAACC

+2 yLeuGluAsp ProGluAspAsp IleCysLys TyrAspPhe ValGluValGlu GluProSe
   -----

541 GCTTGAAGAC CCAGAAGATG ACATATGCAA GTATGATTTT GTAGAAGTTG AGGAACCCAG
   CGAACTTCTG GGTCTTCTAC TGTATACGTT CATACTAAAA CATCTTCAAC TCCTTGGGTC
```

Fig. 9-1



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```
+2 rAspGlyThr IleLeuGlyArg TrpCysGly SerGlyThr ValProGlyLys GlnIleSe
-----
601 TGATGGAAC TATTAGGGC GCTGGTGTGG TTCTGGTACT GTACCAGGAA AACAGATTTCT
    ACTACCTTGA TATAATCCCG CGACCACACC AAGACCATGA CATGGTCCTT TTGTCTAAAG

+2 rLysGlyAsn GlnIleArgIle ArgPheVal SerAspGlu TyrPheProSer GluProGlu
-----
661 TAAAGGAAAT CAAATTAGGA TAAGATTTGT ATCTGATGAA TATTTTCCTT CTGAACCAGG
    ATTTCTTTTA GTTTAATCCT ATTCTAAACA TAGACTACTT ATAAAAGGAA GACTTGGTCC

+2 yPheCysIle HisTyrAsnIle ValMetPro GlnPheThr GluAlaValSer ProSerVal
-----
721 GTTCTGCATC CACTACAACA TTGTCATGCC ACAATTCACA GAAGCTGTGA GTCCTTCAGT
    CAAGACGTAG GTGATGTTGT AACAGTACGG TGTTAAGTGT CTTTCGACACT CAGGAAGTCA

+2 lLeuProPro SerAlaLeuPro LeuAspLeu LeuAsnAsn AlaIleThrAla PheSerThr
-----
781 GCTACCCCTC TCAGCTTTGC CACTGGACCT GCTTAATAAT GCTATAACTG CCTTTAGTAC
    CGATGGGGGA AGTCGAAACG GTGACCTGGA CGAATTATTA CGATATTGAC GGAAATCATG

+2 rLeuGluAsp LeuIleArgTyr LeuGluPro GluArgTrp GlnLeuAspLeu GluAspLeu
-----
841 CTTGGAAGAC CTTATTTCGAT ATCTTGAACC AGAGAGATGG CAGTTGGACT TAGAAGATCT
    GAACCTTCTG GAATAAGCTA TAGAACTTGG TCTCTCTACC GTCAACCTGA ATCTTCTAGA

+2 uTyrArgPro ThrTrpGlnLeu LeuGlyLys AlaPheVal PheGlyArgLys SerArgVal
-----
901 ATATAGGCCA ACTTGGCAAC TTCTTGGCAA GGCTTTTGTT TTTGGAAGAA AATCCAGAGT
    TATATCCGGT TGAACCGTTG AAGAACCGTT CCGAAAACAA AAACCTTCTT TTAGGTCTCA

+2 lValAspLeu AsnLeuLeuThr GluGluVal ArgLeuTyr SerCysThrPro ArgAsnPhe
-----
961 GGTGGATCTG AACCTTCTAA CAGAGGAGGT AAGATTATAC AGCTGCACAC CTCGTAACCT
    CCACCTAGAC TTGGAAGATT GTCTCCTCCA TTCTAATATG TCGACGTGTG GAGCATTGAA

+2 eSerValSer IleArgGluGlu LeuLysArg ThrAspThr IlePheTrpPro GlyCysLeu
-----
1021 CTCAGTGTCC ATAAGGGAAG AACTAAAGAG AACCGATACC ATTTTCTGGC CAGGTTGTCT
    GAGTCACAGG TATTCCCTTC TTGATTCTC TTGGCTATGG TAAAAGACCG GTCCAACAGA

+2 uLeuValLys ArgCysGlyGly AsnCysAla CysCysLeu HisAsnCysAsn GluCysGlu
-----
1081 CCTGGTTAAA CGCTGTGGTG GGAAGTGTGC CTGTTGTCTC CACAATTGCA ATGAATGTCA
    GGACCAATTT GCGACACCAC CCTTGACACG GACAACAGAG GTGTTAACGT TACTTACAGT
```

Fig. 9-2



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```
+2 nCysValPro SerLysValThr LysLysTyr HisGluVal LeuGlnLeuArg ProLysTh
-----
1141 ATGTGTCCCA AGCAAAGTTA CTAAAAAATA CCACGAGGTC CTTCA GTTGA GACCAAAGAC
    TACACAGGGT TCGTTTCAAT GATTTTTTAT GGTGCTCCAG GAAGTCAACT CTGGTTTCTG

+2 rGlyValArg GlyLeuHisLys SerLeuThr AspValAla LeuGluHisHis GluGluCy
-----
1201 CGGTGTCAGG GGATTGCACA AATCACTCAC CGACGTGGCC CTGGAGCACC ATGAGGAGTG
    GCCACAGTCC CCTAACGTGT TTAGTGAGTG GCTGCACCGG GACCTCGTGG TACTCCTCAC

+2 sAspCysVal CysArgGlySer ThrGlyGly
----->
1261 TGA CTGTGTG TGCAGAGGGA GCACAGGAGG ATAGCCGCAT CACCACCAGC AGCTCTTGCC
    ACTGACACAC ACGTCTCCCT CGTGTCTCTC TATCGGCGTA GTGGTGGTCG TCGAGAACGG

1321 CAGAGCTGTG CAGTGCAGTG GCTGATTCTA TTAGAGAACG TATGCGTTAT CTCCATCCTT
    GTCTCGACAC GTCACGTCAC CGACTAAGAT AATCTCTTGC ATACGCAATA GAGGTAGGAA

1381 AATCTCAGTT GTTTGCTTCA AGGACCTTTC ATCTTCAGGA TTTACAGTGC ATTCTGAAAG
    TTAGAGTCAA CAAACGAAGT TCCTGGAAAG TAGAAGTCCT AAATGTCACG TAAGACTTTC

1441 AGGAGACATC AAACAGAATT AGGAGTTGTG CAA
    TCCTCTGTAG TTTGTCTTAA TCCTCAACAC GTT
```

Fig. 9-3



VASCULAR ENDOTHELIAL GROWTH  
FACTOR-X  
Robert D. Gordon, et al.  
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PREDICTED FULL-LENGTH POLYPEPTIDE SEQUENCE

1 MSLFGLLLLT SALAGQRQGT QAESNLSSKF QFSSNKEQYG VQDPQHERII  
51 TVSTNGSIHS PRFPHTYPRN TVLVWRLVAV EENVWIQLTF DERFGLEDPE  
101 DDICKYDFVE VEEPSDGTIL GRWCGSGTVP GKQISKGNQI RIRFVSDEYF  
151 PSEPGFCIHY NIVMPQFTEA VSPSVLPESA LPLDLLNNAI TAFSTLEDLI  
201 RYLEPERWQL DLEDLYRPTW QLLGKAFVFG RKSRVVDLNL LTEEVRLYSC  
251 TPRNFSVSIR EELKRTDTIF WPGCLLVKRC GGNCACCLHN CNECQCVPSK  
301 VTKKYHEVLQ LRPKTGVRGL HKSLTDVALE HHEECDVCR GSTGG

Fig. 10



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ALIGNMENT OF VEGF-X WITH OTHER VEGFs

```

          *          20          *          40          *
VEGF_HUMAN : ----- : -
PLGF_HUMAN : ----- : -
VEGB_HUMAN : ----- : -
VEGC_HUMAN : ----- : -
VEGD_HUMAN : ----- : -
990126vegx : MSLFGLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERII : 50

          60          *          80          *          100
VEGF_HUMAN : ----- : -
PLGF_HUMAN : ----- : -
VEGB_HUMAN : ----- : -
VEGC_HUMAN : ----- : -
VEGD_HUMAN : ----- : -
990126vegx : TVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPE : 100

          *          120          *          140          *
VEGF_HUMAN : ----- : -
PLGF_HUMAN : ----- : -
VEGB_HUMAN : ----- : -
VEGC_HUMAN : -----MHLLGFFSVACSLLAALLPGPREAPAAAA : 30
VEGD_HUMAN : -----MYREWVVNV : 10
990126vegx : DDICKYDFVEV--EEPSDGTILGRWCGSGTVPQKQISKGNQIRIRFVSDE : 148

          160          *          180          *          200
VEGF_HUMAN : -----MN : 2
PLGF_HUMAN : -----MP : 2
VEGB_HUMAN : ----- : -
VEGC_HUMAN : AFESGLDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWK : 80
VEGD_HUMAN : FMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE : 60
990126vegx : YFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLED : 198

          *          220          *          240          *
VEGF_HUMAN : FLLSWVHWSLALLLYLHHAWSQAAPMAEGGGQNHHEVVKFMD-VYORSY : 51
PLGF_HUMAN : VMRLFPCFLQLLAGLALPAVPPQWALSAGNGSSEVEVVPFQE-VWGRSY : 51
VEGB_HUMAN : ---MSPLLRRLLLAALLQLAPAQAPVSQPDAPGHQRKVVSVID-VYTRAT : 46
VEGC_HUMAN : YKQLRKGGWQHNRQANLNSRTEETIKFAAAHYNTEILKSIDNEWRTQ : 130
VEGD_HUMAN : DWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWRTQ : 110
990126vegx : LIRYLEPERWQLLEDLYRPTWQLLGKAFVFGKSRVVDLNLTEEVRLY : 248
```

Fig. 11-1



VASCULAR ENDOTHELIAL GROWTH  
FACTOR-X  
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```
                260          *          280          *          300
VEGF_HUMAN : CHPIETLVDFIQEYPDEIEYIFKPSCVPLMRCG---CCND--EGLECV : 96
PLGF_HUMAN : CRALERLVDDVSEYPSEVEHMFSPSCVSLLRCTG---CCGD--ENLHCVP : 96
VEGB_HUMAN : CQPREVVVPLTVELMGTVAKQLVPSCVTVQRCG---CCPD--DGLECV : 91
VEGC_HUMAN : CMPREVCIDVGKEFGVATNTFFKPPCVSVYRCG---CONS--EGLQCMN : 175
VEGD_HUMAN : CSPRETCVEVASLKGSTNTFFKPPCVNVFRCG---CONE--ESLICMN : 155
990126vegx : SCTPRNFSVSIREELKRTDTIEFWGCLLVKRCGNCACCLHNCNECQCV : 298
```

```
                *          320          *          340          *
VEGF_HUMAN : TEESNTTMDIMRIKPHQG-----QHIGEMSFLOHNKCECRPKKDRARQEK : 141
PLGF_HUMAN : VETANVTMDLKIIRSGDR-----PSYVELTFSQHVRCECRPLREKMKPER : 141
VEGB_HUMAN : TGQHQRMDIILMIRYPS-----SOLGEMSLLEHSQCECRPKKKDSAVKP : 135
VEGC_HUMAN : TSTSLSKTLFEITVPLSQG---PKPVTISFANHTSCROMSKLDVYRQVH : 222
VEGD_HUMAN : TSTSLSKQLFEISVPLTSV---PELVPKVANHTGCKCLFTAPRHPYSI : 202
990126vegx : SKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDVCVRGSTGG--- : 345
```

```
                360          *          380          *          400
VEGF_HUMAN : KSVRGKGGKQKRKRKKSRYKSWSP----- : 166
PLGF_HUMAN : ----- : -
VEGB_HUMAN : DSPR----- : 139
VEGC_HUMAN : SIIRSLPATLPQCAANKTCPTNYMWNHICRLAQEDFMFSSDAGDDS : 272
VEGD_HUMAN : IRRSIQIPEEDRCSHKKLCPIDMLWDSNKCKCVLQENPLAGT----- : 246
990126vegx : ----- : -
```

```
                *          420          *          440          *
VEGF_HUMAN : ----- : -
PLGF_HUMAN : ----- : -
VEGB_HUMAN : ----- : -
VEGC_HUMAN : TDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNK : 322
VEGD_HUMAN : -----EDHSHLQEPALCGP : 260
990126vegx : ----- : -
```

```
                460          *          480          *          500
VEGF_HUMAN : -----CGPCSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNER : 206
PLGF_HUMAN : -----CGDAVPRR----- : 149
VEGB_HUMAN : -----PLCPRCTQHHQRPDPRTCRCRCRRRSFLRCQGRGLELNP : 179
VEGC_HUMAN : LFPSQCGANREFDENTCQCVCKRTCPRNQPLNPGKCACECTESPQKCLLK : 372
VEGD_HUMAN : HMMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLPHPD : 310
990126vegx : ----- : -
```

Fig. 11-2



VASCULAR ENDOTHELIAL GROWTH  
FACTOR-X  
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	*	520	*	540	*
VEGF_HUMAN :	TCRCDKPRR-----				: 215
PLGF_HUMAN :	-----				: -
VEGB_HUMAN :	TCRCRKLRR-----				: 188
VEGC_HUMAN :	GKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCRCVPSYWKRPQMS---				: 419
VEGD_HUMAN :	TCSCEDRCPFHTRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP-----				: 354
990126vegx :	-----				: -

Fig. 11-3



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VARIANT POLYPEPTIDE SEQUENCES

```

      *           20           *           40           *
FL_seq  : MSLFGLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERII : 50
clone41 : MSLFGLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERII : 50
clone20 : MSLFGLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERII : 50

      60           *           80           *           100
FL_seq  : TVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPE : 100
clone41 : TVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPE : 100
clone20 : TVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPE : 100

      *           120           *           140           *
FL_seq  : DDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNQIRIRFVSDEYF : 150
clone41 : DDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNQIRIRFVSDEYF : 150
clone20 : DDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNQIRIRFVSDEYF : 150

      160           *           180           *           200
FL_seq  : PSEPGFCIHYNIIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLI : 200
clone41 : PSEPSNRGGKIIQLHTS----- : 167
clone20 : PSEPGFCIHYNIIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLI : 200

      *           220           *           240           *
FL_seq  : RYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLYSC : 250
clone41 : ----- : -
clone20 : RYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTE----- : 243

      260           *           280           *           300
FL_seq  : TPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP SK : 300
clone41 : ----- : -
clone20 : ----- : -

      *           320           *           340
FL_seq  : VTKKYHEVLQLRPKTGVRGLHKS LTDVALEHHHEECDCVCRGSTGG : 345
clone41 : ----- : -
clone20 : -----EVLQLRPKTGVRGLHKS LTDVALEHHHEECDCVCRGSTGG : 282

```

Fig. 12





VASCULAR ENDOTHELIAL GROWTH  
FACTOR-X  
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PRIMERS FOR EXPRESSION OF VEGF-X

E. coli EXPRESSION OF DOMAIN-

vegx-6 AATTGGATCCGAGAGTGGTGGATCTGAACC

vegx-7 AATTGGATCCGGAAGAAAATCCAGAGTGG

vegx-8 GGTGAATTCATTATTTTTTAGTAACTTTGCTTGGGACAC

vegx-9 AATTGAATTCATTATCCTCCTGTGCTCCCTC

BACULOVIRUS/INSECT CELL EXPRESSION OF FULL-LENGTH PROTEIN-

vegbac1

AATTGGATCCGGAGTCTCACCATCACCACCATCATGAATCCAACCTGAGTAGTAAATTCC

vegbac2

AATTGAATTCGCTATCCTCCTGTGCTCCCTCTGC

Fig. 13



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```
1 >3993180H1  LUNGNON03  INCYTE
2 CACAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGGNGTGTGACTGTGTGTGCAGAGG
3 GAGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTG
4 GCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAG
5 GACCTTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGA
6 GTTGTGCAACAGCTCTTTTGAGAGGAGGCTAAAGGACAGGAGAAANAGGTCTT
7 >3510192H1  CONCNOT01  INCYTE
8 TGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTT
9 GTTTGCTTCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAA
10 ACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGT
11 CTTCAATCGTGGAAAGAAAATTAAATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTT
12 ACCATGTACGTATTCCACTAGCTGGGTTCTGTATTT
13 >2559870H1  ADRETUT01  INCYTE
14 CACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCACCGA
15 CGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGGGGATAGC
16 CGCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGA
17 ACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTTCATCTTCAGG
18 ATTTACAGTGCATTCTGAAAGAGGAGA
19 >3979767H1  LUNGTUT08  INCYTE
20 GGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATT
21 CTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTT
22 CATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGC
23 AACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAN
24 ATTAAATGTTGTATTAAATAGACACCAGCT
25 >3980011H1  LUNGTUT08  INCYTE
26 GGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATT
27 CTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTT
28 CATCTTCAGGATTTACATGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCA
29 ACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAA
30 TTAAATGTTGTATTAAATAGATCACCA
31 >4825396H1  BLADDIT01  INCYTE
32 GAGAACC GATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACTGTG
33 CCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATAC
34 CACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCACCGA
35 CGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGC
36 CGCATCACCA
37 >3073703H1  BONEUNT01  INCYTE
38 AGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCAC
39 ACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGC
40 CAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTCTCCACAATTGCAAT
41 GAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCCTTCAGTTGAGACC
42 AAAGACCGGTGTCAGGGGATTGCACAAATCA
```

Fig. 14-1



27/66

43 >1302516H1 PLACNOT02 INCYTE  
44 AGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCCTTCTGAACCTTCTAACA  
45 GAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACT  
46 AAAGAGAACCGATAACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACT  
47 GTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAA  
48 ATACCACGAGGTCC  
49 >3684109H1 HEANOT01 INCYTE  
50 ATTTTCATCTTCAGGATTTACAGTGCATTCTGAAANAGGAGAAATCAAACANAATTAGGAGTT  
51 GTGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAA  
52 NAAAATTAAATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTC  
53 CACTAGCTGGGTTCTGTATTTTCAGTTCTTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAA  
54 AAAAAGTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTT  
55 >4713188H1 BRAIHCT01 INCYTE  
56 CAAAGTTACTAAAAAATACCACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTCAGGGGAT  
57 TGCACAAATCACTACCGACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGA  
58 GGGAGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCAGAGCTGTGCAGTGCAG  
59 TGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCT  
60 >458823H1 KERANOT01 INCYTE  
61 ANGAGTTGCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCT  
62 CCATCCTTAATCTCAGTTGTTTGNTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCT  
63 TGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTA  
64 AAGGNCAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTAAATGTTGTATTAAATAGATC  
65 >1303909H1 PLACNOT02 INCYTE  
66 AGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCCTTCTGAACCTTCTAACA  
67 GAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACT  
68 AAAGAGAACCGATAACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACT  
69 GTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAG  
70 >2739211H1 OVARNOT09 INCYTE  
71 GTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAG  
72 GAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAGAAAATTAAATGTTGTATTAA  
73 ATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTT  
74 CAGTTCTTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAACTGTGCAAGTGAGCAC  
75 CTGAT  
76 >3325591H1 PTHYNOT03 INCYTE  
77 TGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAG  
78 AAAATTAAATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCC  
79 ACTAGCTGGGTTCTGTATTTTCAGTTCTTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAA  
80 AAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACCCTAAAGCNCCATGTCNNG  
81 GGCNAAAANCGAAAAAT

Fig. 14-2



28/66

82 >3733565H1 SMCCNOS01 INCYTE  
83 CCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGNA  
84 AGANGAGACATCAAACAGAATTAGGNGTTGTGCAAAAGCTCTTTTGAGAGGAGGCCTAAAGG  
85 ACAGGAGAAAAGGTCTNCAATCGTGGAAAGNAAATTAAATGTTGTATNAAATNGATCACCAG  
86 CTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGNCNGTATTCAGTCTTTCGGAAC  
87 GGCTTAGGGTAATGTCAGTACAGGANAAAACTGTGCAGTGAG  
88 >3554223H1 SYNONOT01 INCYTE  
89 ATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTG  
90 TATTTTCAGTTCTTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAACTGTGCAAGTG  
91 AGCACCTGATTCCGTTGCCTTGGCTTAACTCTAAAGCTCCATGTCCTGGGCCTAAAATCGTA  
92 TAAAATCTGGATTTTTTTTNTTTTTTTTTTGCGCATATTCACATATGTAAACCAGNACATTCTA  
93 TGTACNACAAACCTGGTTTTTTAAAAAGGAAC  
94 >4507477H1 OVARTDT01 INCYTE  
95 GGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTTCAGTTCTTTC  
96 GATACGGCTTAGGGTAATGTCAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGT  
97 TGCCTTGCTTAACTCTAAAGCTCCATGTCCTGGGCCTAAAATCGTATAAAATCTGGA  
98 >4163378H1 BRSTNOT32 INCYTE  
99 AATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGNTCTGTATT  
100 TCAGTTCCTTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAAGCTGTGCAAGTGAGC  
101 ACCTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCCATGTCCTGGGCCTAAAATCGTATA

Fig. 14-3



29/66

1 >2054675H1 BEPINOT01 INCYTE  
2 AAAGGAACTATGTTGCTATGAATTAACTTGTGTCGTGCTGATAGGACAGACTGGATTTTTCA  
3 TATTTCTTATTAATAATTTCTGCCATTTAGAAGAAGAGAACTACATTCATGGTTTGGAAGAGAT  
4 AAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATT  
5 GTGTACATTTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATA  
6 TATCTATTTTTTACCAAAGGTATTTAATATTCTTTTTTA  
7 >3993180H1 LUNGNON03 INCYTE  
8 CACAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGGNGTGTGACTGTGTGTGCAGAGGG  
9 AGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGGC  
10 TGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGAC  
11 CTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTG  
12 TGCAACAGCTCTTTTGAGAGGAGGCTAAAGGACAGGAGAAANAGGTCTT  
13 >3510192H1 CONCNOT01 INCYTE  
14 TGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTG  
15 TTTGCTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAAC  
16 AGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCTAAAGGACAGGAGAAAAGGTCTT  
17 CAATCGTGGAAAGAAAATTAAATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCA  
18 TGTACGTATTCCACTAGCTGGGTTCTGTATTT  
19 >4164633H1 BRSTNOT32 INCYTE  
20 CTTGTAAATATATCTATTTTTTACCAAAGGTATTTAATATTCTTTANTTATGACAACTTAGAT  
21 CAACTATTTTTTAGCTTGGTAAATTTTCTAAACACAAATTGTTATAGCCAGAGGAACAAAGATG  
22 ATATAAAATATTGTTGCTCTGACAAAATACATGTATTTTATTCTCGTATGGTGCTAGAGTTA  
23 GATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAAGACTTTTTTGA  
24 NAATAATTAAATTATCATATCTTCCATTCTCTGTTATTGGGGGAGAAAAAT  
25 >2559870H1 ADRETUT01 INCYTE  
26 CACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCACCGAC  
27 GTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGGGGATAGCCG  
28 CATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACG  
29 TATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGATTT  
30 ACAGTGCATTCTGAAAGAGGAGA  
31 >3817470H1 BONSTUT01 INCYTE  
32 TTAAAAAGGAACTATGTTGCTATGAATTAACTTGTGTCATGCTGATAGGACAGACTGGATTT  
33 TTCATATTTCTTATTAATAATTTCTGCCATTTAGAAGAAGAGAACTACATTCATGGTTTGGAAG  
34 AGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTT  
35 CATTGTGTACATTTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTCTAATCTGTTAAA  
36 TATATCTATTTTTTACCAAAGGTATTTAATATTCTTT  
37 >3979767H1 LUNGTUT08 INCYTE  
38 GGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTC  
39 TATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCA  
40 TCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAAC  
41 AGCTCTTTTGAGAGGAGGCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAATTA  
42 AATGTTGTATTAAATAGACACCAGCT

Fig. 15-1



30/66

43 >3980011H1 LUNGTUT08 INCYTE  
44 GGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCAGAGCTGTGCAGTGCAGTGGCTGATTC  
45 TATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCA  
46 TCTTCAGGATTTACATGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACA  
47 GCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAGAAAATTAA  
48 ATGTTGTATTAAATAGATCACCA  
49 >4825396H1 BLADDIT01 INCYTE  
50 GAGAACCGATACCATTTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACCTGTGC  
51 CTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCA  
52 CGAGGTCTTTCAGTTGAGACCAAAGACCGGTGTGAGGGGATTGCACAAATCACTCACCAGCGT  
53 GGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGCA  
54 TCACCACCA  
55 >30737003H1 BONEUNT01 INCYTE  
56 AGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACA  
57 CCTCGTAACCTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTTCTGGCCA  
58 GGTGTCTCCTGGTTAAACGCTGTGGTGGGAACCTGTGCCTGTTGTCTCCACAATTGCAATGAA  
59 TGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCCTTCAGTTGAGACCAAAG  
60 ACCGGTGTGAGGGGATTGCACAAATCA  
61 >862169H1 BRAITUT03 INCYTE  
62 AGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTTCATTCTCGTATGGTGCTAG  
63 AGTTAGATTAATCTGCATTTTAAAAAAGTGAATTGGAATAGAATTGGTAAGTTGCAAAGACTT  
64 TTTGAAAATAATTAAATTATCATATCTTCCATTCTGTTATTGGAGATGAAAATAAAAAGCAA  
65 CTTATGAAAGTAGACATTCAGATCCAGCCATTACTAACCTATTCTTTTTTTGGGGAAATCTGA  
66 GCCTAGC  
67 >4201385H1 BRAITUT29 INCYTE  
68 TTTTTTAAAAGGAACCTATGTTGCTATGAATTAACTTGTGTGCTGCTGATAGGACAGACTGGA  
69 TTTTTTCATATTTCTTATTAAATTTCTGCCATTTAGAAGAAGAGAACTACATTCATGGTTTGG  
70 AAGAGATAAACCTGAAAAGAAGAGTGGCCTATCTTCACTTTATCGATAAGTCAGTTTATTTGT  
71 TTCATTGTGTACATTTTTTATATTCTCCTTTGACATATACTGTTGGCTTTTCTAATCTGTTAA  
72 ATATATCTATTTTTTACCAAAGGTATTTAATAT  
73 >1302516H1 PLACNOT02 INCYTE  
74 AGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCCTTCTGAACCTTCTAACAG  
75 AGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAA  
76 AGAGAACCGATACCATTTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACCTGTG  
77 CCTGTTGTCTCCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATAC  
78 CACGAGGTCC  
79 >3684109H1 HEANOT01 INCYTE  
80 ATTTTCATCTTCAGGATTTACAGTGCATTCTGAAANAGGAGAAATCAAACANAATTAGGAGTTG  
81 TGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAANA  
82 AAATTAAATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCAC  
83 TAGCTGGGTTCTGTATTTTCAGTTCTTTTCGATACGGCTTAGGGTAATGTGAGTACAGGAAAAA  
84 ACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTT

Fig. 15-2



31/66

85 >2549720H1 LUNGTUT06 INCYTE  
86 TTAGCTTGGNAAATTTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAAT  
87 ATTGTTGCTCTGACAAAATAACATGTATTTTCATTCTCGTATGGTGCTAGAGTTAGATTAATCT  
88 GCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAAGACTTTTTGAAAATAATTA  
89 AATTATCATATCTTCCATTCCCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGANAGTAG  
90 >877279H1 LUNGAST01 INCYTE  
91 CTTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGGTAAATTTTTCTAAACACAATTGTT  
92 ATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAATAACATGTATTTTCAT  
93 TCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGG  
94 TAAGTTGCAAAGGCTTTTTGAAAATAATTAAATTATCATATCTTCCATTCCCTGTTATTGGNGG  
95 >4713188H1 BRAIHCT01 INCYTE  
96 CAAAGTTACTAAAAAATACCACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTCAGGGGATT  
97 GCACAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGG  
98 GAGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTGCCCAGAGCTGTGCAGTGCAGTGG  
99 CTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCT  
100 >2171082H1 ENDCNOT03 INCYTE  
101 AGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTT  
102 CATTGTGTACATTTTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTA  
103 AATATATCTATTTTTTACCAAAGGTATTTAATATTCTTTTTTATGACAACCTTAGATCAACTATT  
104 TTTAGCTTGGTAAATTTTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGA  
105 >875860H1 LUNGAST01 INCYTE  
106 CTGGATTTTTTCATATTTCTTATTAATAATTTCTGCCATTTAGAAGAAGAGAACTACATTCATGG  
107 TTTGGAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTT  
108 ATTTGTTTCATTGTGTACATTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAAT  
109 CTTGTAAATATATCTATTTTTTACCAAAGGTATTTAATATTCTTTTTTTATGAC  
110 >706168H1 SYNORAT04 INCYTE  
111 GCTCATATTCACATATGTAAACCAGAACATTTCTATGTACTACAAACCTGGTTTTTAAAAAGGA  
112 NCTATGTTGCTATGAATTAAACTTGTGTCTGTGCTGATAGGACAGACTGGATTTTTTCATATTTT  
113 TTATTAAAATTTCTGCCATTTAGAAGAAGAGAACTACATTCATGGTTTGGAAGAGATAAACCT  
114 GAAAAGAAGAGTGGCCTTATCTTCANTTTATCGATAAGTCAGTTTATTTGTTTCA  
115 >458823H1 KERANOT01 INCYTE  
116 ANGAGTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTC  
117 CATCCTTAATCTCAGTTGTTTGNNTCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTCTG  
118 AAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTAAAG  
119 GNCAGGAGAAAAGGTCTTCAATCGTGGAAGAAAATTAATGTTGTATTAAATAGATC  
120 >538436H1 LNODNOT02 INCYTE  
121 AAAGATGATATAAAATATTGTTGCTCTGACAAAATAACATGTATTTTCATTCTCGTATGGTGCT  
122 AGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAAGAC  
123 TTTTTGAAAATAATTAAATTATCATATCTTCCATTCCCTGTTATTGGAGATGAAAATAAAAAGC  
124 AACTTATGAAAGTAGACATTCAGATCCAGCCATTACTAACCTAT

Fig. 15-3



VASCULAR ENDOTHELIAL GROWTH  
FACTOR-X  
Robert D. Gordon, et al.  
Serial No.: 09/468,647

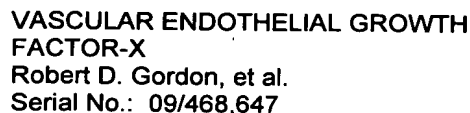
32/66

125 >1303909H1 PLACNOT02 INCYTE  
126 AGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCCTTCTGAACCTTCTAACAG  
127 AGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAA  
128 AGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACGTGTG  
129 CCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAG  
130 >2739211H1 OVARNOT09 INCYTE  
131 GTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGG  
132 AGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAGAAAATTAAATGTTGTATTAAAT  
133 AGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTTCAG  
134 TTCTTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGA  
135 T  
136 >2550343H1 LUNGTUT06 INCYTE  
137 TGTACATTTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCNAATCTTGTTAAATAT  
138 ATCTATTTTTTACCAAAGGTATTTAATATTCTTTTTTATGACAACTTAGATCAACTATTTTTAG  
139 CTTGGTAAATTTTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTG  
140 TTGCTCTGACAAAAATACATGTATTTCAATTCTCGTATGGTGCTA  
141 >5321148H1 FIBPFEN06 INCYTE  
142 CACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGNCAAAAAATACA  
143 TGTATTTTCATTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGA  
144 ATAGAATTGGTAAGTTGCAAAGACTTTTTGAAAATAATTAAATTATCATATCTTCCATTCCTG  
145 TTATTGGAGATGAAAATAAAAAAGCAACTTATGAAAGTAAATTCAGATCCACCATTACTAAC  
146 >879495H1 THYRNOT02 INCYTE  
147 ATTTCAATTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATA  
148 GAATTGGTAAGTTGCAAAGACTTTTTGAAAATAATTAAATTATCATATCTTCCATTCCTGTTA  
149 TTGGAGATGAAAATAAAAAAGCAACTTATGAAAGTAGACATTCAGATCCAGCCATTACTAACCT  
150 ATTCCTTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAGCACCTTGAAAAA  
151 >3325591H1 PTHYNOT03 INCYTE  
152 TGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAGA  
153 AAATTAAATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCAC  
154 TAGCTGGGTTCTGTATTTTCAGTTCCTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAA  
155 ACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACCTAAAGCNCCATGTCNNGGGCN  
156 AAAANCGAAAAAT  
157 >543890H1 OVARNOT02 INCYTE  
158 TTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACA  
159 AAAATACATGTATTTTCATTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACT  
160 GAATTGGNATAGAATTGGTAAGTTGCAAAGNCTTTTTGAAAATAATTAAATTATCATATCTTC  
161 CATTCTGTTATTGGAGGATGGAAAATAAAAAAGCAACTTATGGAAAGTAGGACATTTCAGATC  
162 >3733565H1 SMCCNOS01 INCYTE  
163 CCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGNAA  
164 GANGAGACATCAAACAGAATTAGGNGTTGTGCAAAAGCTCTTTTGAGAGGAGGCCTAAAGGAC  
165 AGGAGAAAAGGTCTNCAATCGTGGAAGNAAATTAAATGTTGTATNAAATNGATCACCAGCTA  
166 GTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGNCNGTATTTCAGTCTTTCGGAACGGCT  
167 TAGGGTAATGTCAGTACAGGANAAAACTGTGCAGTGAG

Fig. 15-4







211 >1955646H1 CONNNOT01 INCYTE  
212 TGGTAAGTTGCAAAGACTTTTTGAAAATAATTAAATTATCATATCTTCCATTTCCTGTTATTGG  
213 AGATGAAAATAAAAAAGCAACTTATGAAAGTAGACATTTCAGATCCAGCCATTACTAACCTATTTC  
214 CTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAGCACCTTGAAAAAGACTTGGCA  
215 GCTTCCTGATAAAGCGTGCTGTGCTGTGCAGTAGGGAACACATCCTATTTATTGTGATGTTGT  
216 GGTTTATATCCTAAACC  
217 >4163378H1 BRSTNOT32 INCYTE  
218 AATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCA TAGCTGGGNTCTGTATTT  
219 CAGTTCCTTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAGCTGTGCAAGTGAGCAC  
220 CTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCCATGTCCTGGGCCTAAATCGTATA  
221 >5095141H1 EPIMNON05 INCYTE  
222 AGATAAACCTGAAAAGAAGAGTGGCCTTATNTTCACTTTATCGATAAGTCAGNTTATTTGTTT  
223 CATTGTGTACATTTNNATATTCTCCTTTTGACATTATAACTGNTGGCTTTTCTAANCNTGTTA  
224 AATATATCTATTTTTACCAAAGGTATTTAATATTCTTT  
225 >943826H1 ADRENOT03 INCYTE  
226 TATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGT  
227 TGCAAAGACTTTTTGAAAATAATTAAATTATCATATCTTCCATTTCCTGTTATTGGAGATGAAA  
228 ATAAAAAGCAACTTATG  
229 >3451273H1 UTRSNON03 INCYTE  
230 TTTTTTNTTTTGCTCATATTCACATATGTAAACCNGAACATTCTATGTACNACAAACCTGGTT  
231 TTTAAAAAGGAACTATGTTGCTATGAATTAAACTTGTGTCGTGCTGATAGGACAGACTGGATT  
232 TTTCANATTTCTTANTAANNTTTCTGCCATTTAGAAGA  
233 >1402278H1 LATRTUT02 INCYTE  
234 GTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACTCTAAAGCTC  
235 CATGTCCTGGGCCTAAATCGTATAAAATCTGGAnnnnnnnnnnnnnnnnnnnnGCTCATATTCA  
236 CATATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCT  
237 ATGAATTAAACTTGTGTCGTGCTGATAGGACAGACTGGATTTTTTCATATTTCTTA  
238 >4361191H1 SKIRNOT01 INCYTE  
239 GCAAAGACTTTTTGANAA TNATTAANTTATCATATCTTCCATTTCCTGTTATNGGAGATGANAA  
240 TAAAAAGCAACTTATGAAAGTAGACATTTCAGATCCAGCCATTACTAACCTATTCCTTTTTTGG  
241 GGAAATCTGAGCCTAGCNCAGAAAAACATAAAGCACCTTGAAAAAGACTTGGCAGCTTCCTGA  
242 TAAAGCGTGCTGTGCTGTGCAGTAGGAACACATCCNATTTATTGTGNTGTNGNGGTTTTATGA  
243 TC  
244 >1307017H1 PLACNOT02 INCYTE  
245 TGTCAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACTCTAA  
246 AGCTCCATGTCCTGGGCCTAAATCGTATAAAATCTGGAnnnnnnnnnnnnnnnnnnnnGCTCAT  
247 ATTACATATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATG  
248 TTGCTATGAATTAAACTTGTGTGTCATGCTGATAGGACAGACTGGATTTTTTCATAT  
249 >5032225H1 HEARFET03 INCYTE  
250 AATTATCATATCTTCCATTTCCTGTTATTGGAGATGNAAATAAAAAAGCAACTTATGAAAGTAGA  
251 CATTTCAGATCCAGCCATTACTAACCTATTCCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAA  
252 AACATAAAGCACCTTGAAAAAGACTGTCAGCTTCCTGATAAAGCGTGCTGTGCTGTGCAGTAG  
253 GAACACATCCTATTTATTGTGATGTTGTGGTTTTATTATCTTAAACTCGTTCCAT

**Fig. 15-6**



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254 >3732621H1 SMCCNOS01 INCYTE  
255 ANAGATGATATAAAANATTGTTGCTCTGACAANNATACATGTATTTTCATTCTCGTATGGTGCT  
256 AGAGTTAGATTAATCTGCNTTTTAAAAAACTGANTTGAATAGANTTGGTAAGTTGCAAAGNC  
257 NTTTGAAAATNATTAAGTTATCAGAT  
258 >3530274H1 BLADNOT09 INCYTE  
259 TTCCATTCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGAAAGTAGACATTCAGATCCA  
260 GCCATTACTAACCTATTCCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAGCAC  
261 CTTGAAAAAGACTTGGCAGCTTCCTGATAAAGCGTGCTGTGCTGTGCAGTAGGAACACATCCT  
262 ATTTATTGTGATGTTGTGGTTTTATTATCTAAACTCTGTTCCATACACTTGTATAAATACATG  
263 GATATTTTTTATGTACAGAAGTATGTCTCTTAACCAAGTTCA  
264 >3530249H1 BLADNOT09 INCYTE  
265 CTTCCATTCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGANAGTAGACATTCAGATCC  
266 AGCCATTACTAACCTATTCCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAGCA  
267 CTTGAAAAAGACTTGGCAGCTTCCTGATAAAGCGTGCTGTGCTGTGCAGTAGGAACACATCC  
268 TATTTATTGTGATGTTGTGGTTTTATTATCTTAAACTCTGTTCCATACACTTGTATAAATACA  
269 TGGATATTTTTTATGTACAGAAGTATGTCTCTTAACCAAGTTCACTTATTGTACCTGG

Fig. 15-7



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VEGFE1	AAAATGTATGGATACAACTTAC	22
VEGFE2	GTTTGATGAAAGATTTGGGCTTG	23
VEGFE3	TTTCTAAAGGAAATCAAATTAG	22
VEGFE4	GATAAGATTTGTATCTGATG	20
VEGFE5	GATGTCTCCTCTTTTCAG	17
VEGFE6	GCACAACTCCTAATTCTG	18
VEGFE7	AGCACCTGATTCCGTTGC	19
VEGFE8	TAGTACATAGAATGTTCTGG	20
VEGFE9	AAGAGACATACTTCTGTAC	19
VEGFE10	CCAGGTACAATAAGTGAAGTGA	21

Fig. 16



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```
+3           M N I F L L N L L T E E V R L Y
              ]-----
1  AGGAAATCAA ATTAGGATAA GATTGTATC TGATGAATAT TTTCCTTCTG AACCTTCTAA CAGAGGAGGT AAGATTATAC
   TCCTTTAGTT TAATCCTATT CTAAACATAG ACTACTTATA AAAGGAAGAC TTGGAAGATT GTCTCCTCCA TTCTAATATG

+3  S C T P R N F S V S I R E E L K R T D T I F W P G C L
      -----]-----
81  AGCTGCACAC CTCGTAACCT CTCAGTGTCC ATAAGGGAAG AACTAAAGAG AACCGATACC ATTTTCTGGC CAGGTTGTCT
   TCGACGTGTG GAGCATTGAA GAGTCACAGG TATTCCCTTC TTGATTCTC TTGGCTATGG TAAAGACCG GTCCAACAGA
-2                                     <-----

+3  L V K R C G G N C A C C L H N C N E C Q C V P S K V
      -----
161 CCTGGTTAAA CGCTGTGGTG GGAAGTGTGC CTGTTGTCTC CACAATTGCA ATGAATGTCA ATGTGTCCCA AGCAAAGTTA
   GGACCAATTT GCGACACCAC CCTTGACACG GACAACAGAG GTGTTAACGT TACTTACAGT TACACAGGGT TCGTTTCAAT
-2 -----

+3  T K K Y H E V L Q L R P K T G V R G L H K S L T D V A
      -----
+1                                     V S G D C T N H S P T W P
                                      ]-----
241 CTAAAAAATA CCACGAGGTC CTTCACTTGA GACCAAAGAC CGGTGTCAGG GGATTGCACA AATCACTCAC CGACGTGGCC
   GATTTTTTAT GGTGCTCCAG GAAGTCAACT CTGGTTTCTG GCCACAGTCC CCTAACGTGT TTAGTGAGTG GCTGCACCGG
-2 -----[

+3  L E H H E E C D C V C R G S T G G
      ----->
+2                                     V Q R E H R R I A A S P P A A L A
                                      ]-----
+1  W S T M R S V T V C A E G A Q E D S R I T T S S S C
      -----
321 CTGGAGCACC ATGAGGAGTG TGAAGTGTG TGCAGAGGGA GCACAGGAGG ATAGCCGCAT CACCACCAGC AGCTCTTGCC
   GACCTCGTGG TACTCCTCAC ACTGACACAC ACGTCTCCCT CGTGTCTCTC TATCGGCGTA GTGGTGGTCG TCGAGAACGG

+2  Q S C A V Q W L I L L E N V C V I S I L N L S C L L Q
      -----
+1  P E L C S A V A D S I R E R M R Y L H P
      ----->
401 CAGAGCTGTG CAGTGCAGTG GCTGATTCTA TTAGAGAACG TATGCGTTAT CTCCATCCTT AATCTCAGTT GTTTGCTTCA
   GTCTCGACAC GTCACGTCAC CGACTAAGAT AATCTCTTGC ATACGCAATA GAGGTAGGAA TTAGAGTCAA CAAACGAAGT
```

Fig. 17-1



VASCULAR ENDOTHELIAL GROWTH  
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+2 G P F I F R I Y S A F

----->

481 AGGACCTTTC ATCTTCAGGA TTTACAGTGC ATTCTGAAAG AGGAGACATC AAACAGAATT AGGAGTTGTG CAACAGCTCT  
TCCTGGAAAG TAGAAGTCCT AAATGTCACG TAAGACTTTC TCCTCTGTAG TTTGTCTTAA TCCTCAACAC GTTGTGCGAGA

561 TTTGAGAGGA GGCCTAAAGG ACAGGAGAAA AGGTCTTCAA TCGTGGAAG AAAATTAAAT GTTGTATTAA ATAGATCACC  
AAACTCTCCT CCGGATTTC TGTCTCTTT TCCAGAAGTT AGCACCTTTC TTTTAATTTA CAACATAATT TATCTAGTGG

641 AGCTAGTTTC AGAGTTACCA TGTACGTATT CCACTAGCTG GGTCTGTAT TTCAGTTCTT TCGATACGGC TTAGGGTAAT  
TCGATCAAAG TCTCAATGGT ACATGCATAA GGTGATCGAC CCAAGACATA AAGTCAAGAA AGCTATGCCG AATCCCATT

721 GTCAGTACAG GAAAAAACT GTGCAAGTGA GCACCTGATT CCGTTGCCTT GGCTTAACTC TAAAGCTCCA TGTCTGGGC  
CAGTCATGTC CTTTTTTTGA CACGTTCACT CGTGGAATAA GGCAACGGAA CCGAATTGAG ATTTGAGGT ACAGGACCCG

801 CTAAAATCGT ATAAAATCTG GA  
GATTTTAGCA TATTTTAGAC CT

Fig. 17-2



VASCULAR ENDOTHELIAL GROWTH  
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```
+3          M N I F L L N L L T E E V R L Y
          ]-----
1  AGGAAATCAA ATTAGGATAA GATTGTATC TGATGAATAT TTCCTTCTG AACCTTCTAA CAGAGGAGGT AAGATTATAC
   TCCTTTAGTT TAATCCTATT CTAAACATAG ACTACTTATA AAAGGAAGAC TTGGAAGATT GTCTCCTCCA TTCTAATATG

+3  S C T P R N F S V S I R E E L K R T D T I F W P G C L
   -----]-----
81 AGCTGCACAC CTCGTAACCT CTCAGTGTCC ATAAGGGAAG AACTAAAGAG AACCGATACC ATTTTCTGGC CAGGTTGTCT
   TCGACGTGTG GAGCATTGAA GAGTCACAGG TATTCCCTTC TTGATTCTC TTGGCTATGG TAAAGACCG GTCCAACAGA
-2          <-----

+3  L V K R C G G N C A C C L H N C N E C Q C V P S K V
   -----
161 CCTGGTTAAA CGCTGTGGTG GGAAGTGTGC CTGTTGTCTC CACAATTGCA ATGAATGTCA ATGTGTCCCA AGCAAAGTTA
   GGACCAATTT GCGACACCAC CCTTGACACG GACAACAGAG GTGTTAACGT TACTTACAGT TACACAGGGT TCGTTTCAAT
-2 -----

+3  T K K Y H E V L Q L R P K T G V R G L H K S L T D V A
   -----
+1          V S G D C T N H S P T W P
          ]-----
241 CTAAAAAATA CCACGAGGTC CTTCAAGTTGA GACCAAAGAC CGGTGTCAGG GGATTGCACA AATCACTCAC CGACGTGGCC
   GATTTTTTAT GGTGCTCCAG GAAGTCAACT CTGGTTTCTG GCCACAGTCC CCTAACGTGT TTAGTGAGTG GCTGCACCGG
-2 -----[

+3  L E H H E E C D C V C R G S T G G
   ----->
+2          V Q R E H R R I A A S P P A A L A
          ]-----
+1  W S T M R S V T V C A E G A Q E D S R I T T S S S C
   -----
321 CTGGAGCACC ATGAGGAGTG TGAAGTGTG TGCAGAGGGA GCACAGGAGG ATAGCCGCAT CACCACCAGC AGCTCTTGCC
   GACCTCGTGG TACTCCTCAC ACTGACACAC ACGTCTCCCT CGTGTCTCTC TATCGGCGTA GTGGTGGTCG TCGAGAACGG

+2  Q S C A V Q W L I L L E N V C V I S I L N L S C L L Q
   -----
+1  P E L C S A V A D S I R E R M R Y L H P
   ----->
401 CAGAGCTGTG CAGTGCAGTG GCTGATTCTA TTAGAGAACG TATGCGTTAT CTCCATCCTT AATCTCAGTT GTTTGCTTCA
   GTCTCGACAC GTCACGTCAC CGACTAAGAT AATCTCTTGC ATACGCAATA GAGGTAGGAA TTAGAGTCAA CAAACGAAGT
```

Fig. 18-1



VASCULAR ENDOTHELIAL GROWTH  
FACTOR-X  
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+2 G P F I F R I Y S A F  
----->

481 AGGACCTTTC ATCTTCAGGA TTTACAGTGC ATTCTGAAAG AGGAGACATC AAACAGAATT AGGAGTTGTG CAACAGCTCT  
TCCTGGAAAG TAGAAGTCCT AAATGTCACG TAAGACTTTC TCCTCTGTAG TTTGTCTTAA TCCTCAACAC GTTGTGCGAGA

561 TTTGAGAGGA GGCCTAAAGG ACAGGAGAAA AGGTCTTCAA TCGTGGAAAG AAAATTAAAT GTTGATTAA ATAGATCACC  
AAACTCTCCT CCGGATTTCC TGTCTCTTT TCCAGAAATT AGCACCTTTC TTTTAATTTA CAACATAATT TATCTAGTGG

641 AGCTAGTTTC AGAGTTACCA TGTACGTATT CCACTAGCTG GGTTCGTAT TTCAGTTCTT TCGATACGGC TTAGGGTAAT  
TCGATCAAAG TCTCAATGGT ACATGCATAA GGTGATCGAC CCAAGACATA AAGTCAAGAA AGCTATGCCG AATCCCATTA

721 GTCAGTACAG GAAAAAACT GTGCAAGTGA GCACCTGATT CCGTTGCCTT GGCTTAACTC TAAAGCTCCA TGTCTGGGC  
CAGTCATGTC CTTTTTTTGA CACGTTCACT CGTGGACTAA GGCAACGGAA CCGAATTGAG ATTTGAGGT ACAGGACCCG

801 CTAAAAATCGT ATAAAAATCTG GATTTTTTTN TTTTTTTTG CGCATATTCA CATATGTAAA CCAGAACATT CTATGTACTA  
GATTTTAGCA TATTTTAGAC CTAAAAAAN AAAAAAAC GCGTATAAGT GTATACATTT GGTCTGTAA GATACATGAT

881 CAAACCTGGT TTTTAAAAG GAACTATGTT GCTATGAATT AAACCTGTGT CGTGCTGATA GGACAGACTG GATTTTTCAT  
GTTTGGACCA AAAATTTTTC CTTGATACAA CGATACTTAA TTTGAACACA GCACGACTAT CCTGTCTGAC CTAAAAAGTA

-3 <-----

961 ATTTCTTATT AAAATTTCTG CCATTAGAA GAAGAGAACT ACATTCATGG TTTGGAAGAG ATAAACCTGA AAAGAAGAGT  
TAAAGAATAA TTTTAAAGAC GGTAAATCTT CTTCTCTTGA TGTAAGTACC AAACCTTCTC TATTTGGACT TTTCTTCTCA

-3 -----

1041 GGCCTTATCT TCACTTTATC GATAAGTCAG TTTATTTGTT TCATTGTGTA CATTTTATA TTCTCCTTTT GACATTATAA  
CCGGAATAGA AGTGAAATAG CTATTCAGTC AAATAAACAA AGTAACACAT GTAAAAATAT AAGAGGAAAA CTGTAATATT

-3 ----- [

1121 CTGTTGGCTT TTCTAATCTT GTTAAATATA TCTATTTTTC CCAAAGGTAT TTAATATTCT TTTTATGAC AACTTAGATC  
GACAACCGAA AAGATTAGAA CAATTTATAT AGATAAAAAT GGTTCCTATA AATTATAAGA AAAAATACTG TTGAATCTAG

1201 AACTATTTT AGCTTGGTAA ATTTTCTAA ACACAATTGT TATAGCCAGA GGAACAAAGA TGATATAAAA TATTGTTGCT  
TTGATAAAA TCGAACCATT TAAAAGATT TGTGTTAACA ATATCGGTCT CCTTGTTTCT ACTATATTTT ATAACAACGA

1281 CTGACAAAA TACATGTATT TCATTCTCGT ATGGTGCTAG AGTTAGATTA ATCTGCATTT TAAAAAATG AATTGGAATA  
GACTGTTTT ATGTACATAA AGTAAGAGCA TACCACGATC TCAATCTAAT TAGACGTAAA ATTTTTTGAC TTAACCTTAT

1361 GAATTGGTAA GTTGCAAAGA CTTTTGAAA ATAATTAAAT TATCATATCT TCCATTCCTG TTATTGGAGA TGAAAAATAA  
CTTAACCATT CAACGTTTCT GAAAACTTT TATTAATTTA ATAGTATAGA AGGTAAGGAC AATAACCTCT ACTTTTATTT

Fig. 18-2





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1441 AAGCAACTTA TGAAAGTAGA CATTGAGATC CAGCCATTAC TAACCTATTC CTTTTTTGGG GAAATCTGAG CCTAGCTCAG  
TTCGTTGAAT ACTTTCATCT GTAAGTCTAG GTCGGTAATG ATTGGATAAG GAAAAAAGCC CTTTAGACTC GGATCGAGTC

1521 AAAACATAA AGCACCTTGA AAAAGACTTG GCAGCTTCCT GATAAAGCGT GCTGTGCTGT GCAGTAGGAA CACATCCTAT  
TTTTTGATTT TCGTGGAAGT TTTTCTGAAC CGTCGAAGGA CTATTTTCGA CGACACGACA CGTCATCCTT GTGTAGGATA

1601 TTATTGTGAT GTTGTGGTTT TATTATCTTA AACTCTGTTC CATACTTGT TATAAATACA TGGATATTTT TATGTACAGA  
AATAACACTA CAACACCAA ATAATAGAAT TTGAGACAAG GTATGTGAAC ATATTTATGT ACCTATAAAA ATACATGTCT

1681 AGTATGTCTC TTAACCAGTT CACTTATTGT ACCTGG  
TCATACAGAG AATTGGTCAA GTGAATAACA TGGACC

Fig. 18-3



42/66

DNA AND POLYPEPTIDE SEQUENCE USED FOR MAMMALIAN CELL EXPRESSION

```
+1      m s l f g l l l l t s a l a g q r
1      GGATCCAAAA TGAGCCTCTT CGGGCTTCTC CTGCTGACAT CTGCCCTGGC CGGCCAGAGA

+1      q g t q a E S N L S S K F Q F S S N K E
61     CAGGGGACTC AGGCGGAATC CAACCTGAGT AGTAAAGTTC CAGTTTTCCTA GCAACAAGGA

+1      Q N G V Q D P Q H E R I I T V S T N G S
121    ACAGAACGGA GTACAAGATC CTCAGCATGA GAGAATTATT ACTGTGTCTA CTAATGGAAG

+1      I H S P R F P H T Y P R N T V L V W R L
181    TATTCACAGC CCAAGGTTTC CTCATACTTA TCCAAGAAAT ACGGTCTTGG TATGGAGATT

+1      V A V E E N V W I Q L T F D E R F G L E
241    AGTAGCAGTA GACGAAAATG TATGGATACA ACTTACGTTT GATGAAAGAT TTGGGCTTGA

+1      D P E D D I C K Y D F V Z V E E P S D G
301    AGACCCAGAA GATGACATAT GCAAGTATGA TTTTGTAGAA GTTGACAAAC CCAGTGATGG

+1      T I L G R W C G S G T V P G K Q I S K G
361    AACTATATTA GGGCCCTGGT GTGGTTCTGG TACTGTACCA GGAAAACAGA TTTCTAAAGG

+1      N Q I R I R F V S D E Y F P S E P G F C
421    AAATCAAATT AGGATAAGAT TTGTATCTGA TGAATATTTT CCTTCTGPAC CAGGGTTCTG

+1      I H Y N I V M P Q F T E A V S P S V L P
481    CATCCACTAC AACATTGTCA TGCCACAATT CACAGAAGCT GTGAGTCCTT CAGTGCTACC

+1      P S A L P L D L L N N A I T A F S T L E
541    CCCTTCAGCT TTGCCACTTG GACCTGCTTA ATAATGCTAT AACTGCCTTT AGTACCTTCG

+1      D L I R Y L E P E R W Q L D L E D L Y R
601    AAGACCTTAT TCGATATCTT GAACCAGAGA GXTGGCAGTT GGACTTAGAA GATCTATATA

+1      P T W Q L L G K A F V F G R K S R V V D
661    GGCCAACTTG GCAACTTCTT GGCAAGGCTT TTGTTTTTGG AAGAAAATCC AGAGTGGTGG

+1      L N L L T E E V R L Y S C T P R N F S V
721    ATCTGAACCT TCTAACAGAG GAGGTAAGXT TATACAGCTG CACACCTCGT AACTTCTCAG

+1      S I R E E L K R T D T I F W P G C L L V
781    TGTCCATAAG GGAAGAACTT AAAGAGAACC GATACCATTT TCTGGCCAGG TTGTCTCCTG
```

Fig. 19-1



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+1    K R C G    G N C    A C C    L H N C    N E C    Q C V  
841   GTTAAACGCT GTGGTGGGAA CTGTGCCTGT TGTCTCCACA ATTGCAATGA ATGTCAATGT

+1    P S K V    T K K    Y H E    V L Q L    R P K    T G V  
901   GTCCCAAGCA AAGTTACTAA AAAATACCAC GAGGTCCTTC AGTTGAGACC AAAGACCGGT

+1    R G L H    K S L    T D V    A L E H    H E E    C G C  
961   GTCAGGGGAT TGCACAAATC ACTCACCGAC GTGGCCCTGG AGCACCATGA GGAGTGTGAC

+1    V C R G    S T G    G S R    G P F E    C K P    I P N  
1021 TGTGTGTGCA GAGGGAGCAC AGGAGGATCT AGAGGGCCCT TCGAAGGTAA GCCTATCCCT

+1    P L L G    L D S    T R T    G H H H    H H H  
1081 AACCTCTCC TCGGTCTCGA TTCTACGCGT ACCGGTCATC ATCACCATCA CCATTGA

Fig. 19-2



VASCULAR ENDOTHELIAL GROWTH  
FACTOR-X  
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DNA AND POLYPEPTIDE SEQUENCE USED FOR BACULOVIRUS/INSECT CELL EXPRESSION

```
1      GAATTCAAAG GCCTGTATTT TACTGTTTTC GTAACAGTTT TGTAATAAAA AAACCTATAA
+3      m k f l v n v a l v f m v v y i s y i
61      ATATGAAATT CTTAGTCAAC GTTGCCCTTG TTTTATGGT CGTATACATT TCTTACATCT
+3      y a D P E S H H H H H E S N L S S K F
121     ATGCGGATCC GGAGTCTCAC CATCACCACC ATCATGAATC CAACCTGAGT AGTAAATTCC
+3      Q F S S N K E Q N G V Q D P Q H E R I I
181     AGTTTTCCAG CAACAAGGAA CAGAACGGAG TACAAGATCC TCAGCATGAG AGAATTATTA
+3      T V S T N G S I H S P R F P H T Y P R N
241     CTGTGTCTAC TAATGGAAGT ATTCACAGCC CAAGGTTTCC TCATACTTAT CCAAGAAATA
+3      T V L V W R L V A V E E N V W I Q L T F
301     CGGTCTTGGT ATGGAGATTA GTAGCAGTAG AGGAAAATGT ATGGATACAA CTTACGTTTG
+3      D E R F G L E D P G D D I C K Y D F V G
361     ATGAAAGATT TGGGCTTGAA GACCCAGAAG ATGACATATG CAAGTATGAT TTTGTAGAAG
+3      V E E P S D G T I L G R W C G S G T V P
421     TTGAGGAACC CAGTGATGGA ACTATATTAG GGCGCTGGTG TGGTCTGGT ACTGTACCAG
+3      G K E I S K G N Q I R I R F V S D E Y F
481     GAAAACAGAT TTCTAAAGGA AATCAAATTA GGATAAGATT TGTATCTGAT GAATATTTTC
+3      P S E P G F C I H Y N I V M P Q F T E A
541     CTTCTGAACC AGGGTTCTGC ATCCACTACA ACATTGTCAT GCCACAATTC ACAGAAGCTG
+3      V S P S V L P P S A L P L D L L N N A I
601     TGAGTCCTTC AGTGCTACCC CCTTCAGCTT TGCCACTGGA CCTGCTTAAT AATGCTATAA
+3      T A F S T L E D L I R Y L E P E R W Q L
661     CTGCCTTTAG TACCTTGGA GACCTTATTC GATATCTTGA ACCAGAGAGA TGGCAGTTGG
+3      D L E D L Y R P T W Q L L G K A F V F G
721     ACTTAGAAGA TCTATATAGG CCAACTTGGC AACTTCTTGG CAAGGCTTTT GTTTTTTGAA
```

Fig. 20-1



VASCULAR ENDOTHELIAL GROWTH  
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```
+3   R K S R V V D L R L L T E E V R L Y S C  
781  GAAAATCCAG AGTGGTGGAT CTGAACCTTC TAACAGAGGA GGTAAGATTA TACAGCTGCA  
  
+3   T P R N F S V S I R E E L K R T D T I F  
841  CACCTCGTAA CTTCTCAGTG TCCATAAGGG AAGAATAAA GAGAACCGAT ACCATTTTCT  
  
+3   W P G C L L V K R C G G N C A C C L H N  
901  GGCCAGGTTG TCTCCTGGTT AAACGCTGTG GTGGGAACTG TGCCTGTTGT CTCCACAATT  
  
+3   C N E C Q C V P S K V T K K Y H E V L Q  
961  GCAATGAATG TCAATGTGTC CCAAGCAAAG TTACTAAAAA ATACCACGAG GTCCTTCAGT  
  
+3   L R P K T G V R G L H K S L T D V A L E  
1021 TGAGACCAAA GACCGGTGTC AGGGGATTGC ACAAATCACT CACCGACGTG GCCCTGGAGC  
  
+3   H H E E C D C V C R G S T G G  
1081 accatgagga gtgtgactgt gtgtgcagag ggagcacagg aggatagctc taga
```

Fig. 20-2



VASCULAR ENDOTHELIAL GROWTH  
FACTOR-X  
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DNA AND POLYPEPTIDE SEQUENCE USED FOR E.coli EXPRESSION

+ 3     Q T N S S S N N N N N N N N N L G I  
1     CGCAGACTAA TTCGAGCTCG AACAAACAACA ACAATAACAA TAACAACAAC CTCGGGATCG  
  
      E G R I S E F E S N L S S K F Q F S S N  
61     AGGGAAGGAT TTCAGAATTC GAATCCAACC TGAGTAGTAA ATTCCAGTTT TCCAGCAACA  
  
+ 3     K E Q N G V Q D P Q H E R I I T V S T N  
121     AGGAACAGAA CCGAGTACAA GATCCTCAGC ATGAGAGAAT TATTACTGTG TCTACTAATG  
  
+ 3     G S I H S P R F P H T Y P R N T V L V W  
181     GAAGTATTCA CAGCCCAAGG TTTCTCATA CTTATCCAAG AAqTACGGTC TTGGTATGGA  
  
+ 3     R L V A V E E N V W I Q L T I D E R F G  
241     GATTAGTXGC AGTAGAGGAA AATGTATGGA TACAACCTAC GTTTGATGAA AGATTTGGGC  
  
+ 3     L E D P E D D I C K Y D F V E V E E P S  
301     TTGAAGACCC AGAAGATGAC ATATGCAAGT ATGATTTTGT AGAAGTTGAG GAACCCAGTG  
  
+ 3     D G T I L G R W C G S G T V P G K Q I S  
361     ATGGAACATAT ATTAGGGCGC TGGTGTGGTT CTGGTACTGT ACCAGGAAAA CAGATTTCTA  
  
+ 3     K G S Q I R I R F V S D E Y F P S E P G  
421     AAGGAAATCA AATTAGGATA AGATTTGTAT CTGATGAATA TTTTCCTTCT GAACCAGGGT  
  
+ 3     F C I H Y N I V M P Q F T E A V S P S V  
481     TCTGCATCCA CTACAACATT GTCATGCCAC AATTCACAGA AGCTGTGAGT CCTTCAGTGC  
  
+ 3     L P P S A L P L D L L N N A I T A F S T  
541     TACCCCTTC AGZTTTGCCA CTGGACCTGC TTAATAATGC TATAACTGCC TTAGTACCT  
  
+ 3     L E D L I R Y L E P E R W Q L D L E D L  
601     TGGAAGACCT TATTCGATAT CTTGAACCAG AGAGATGGCA GTTGACTTA GAAGATCTAT  
  
+ 3     Y R P T W Q L L G K A F V F G R K S R V  
661     ATAGGCCAAC TTGGCAACTT CTTGGCAAGG CTTTTGTTTT TGGAAGAAAA TCCAGAGTGG  
  
+ 3     V D L N L L T E E V R L Y S C T P R N F  
721     TGGATCCGAA CCTTCTAACA GAGGAGGTAA GATTATACAG CTGCACACCT CGTAACTTCT  
  
+ 3     S V S I R E E L K R T D T I F W P G C L  
781     CAGTGTCCAT AAGGGAAGAA CTAAAGAGAA CCGATACCAT TTTCTGGCCA GTTTGTCTCC

Fig. 21-1



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+ 3 L V K R C G G N C A C C L E N C N E C Q  
841 TGGTTAAACG CTGCGGTGGG AACTGTGCCT GTTGTCTCCA CAATTGCAAT GAATGTCAAT

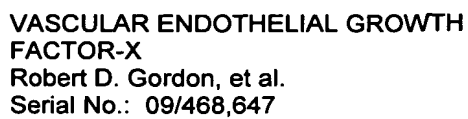
+ 3 C V I S K V T K K Y H E V L Q L R P K T  
901 GTGTCCCAAG CAAAGTTACT AAAAAATACC ACGAGGTCCT TCAGTTGAGA CCAAAGACCG

+ 3 G V R G L H K S L T D V A L E H H E E C  
961 GTGTCAGGGG ATTGCACAAA TCACTCACCG ACGTGGCCCT GGAGCACCAT GAGGAGTGTG

+ 3 D C V C R G S T G G H H H H H H \*  
1021 ACTGTGTGTG CAGAGGGAGC ACAGGAGGAC ATCATCACCA TCACCATTGA TCTAGAGTCG

1081 ACCTGCAGGC AAGCTT

Fig. 21-2

[illegible]

**E.coli EXPRESSION**

M                    +                    -

← PUTATIVE DIMER

← MONOMER

**Fig. 22B**





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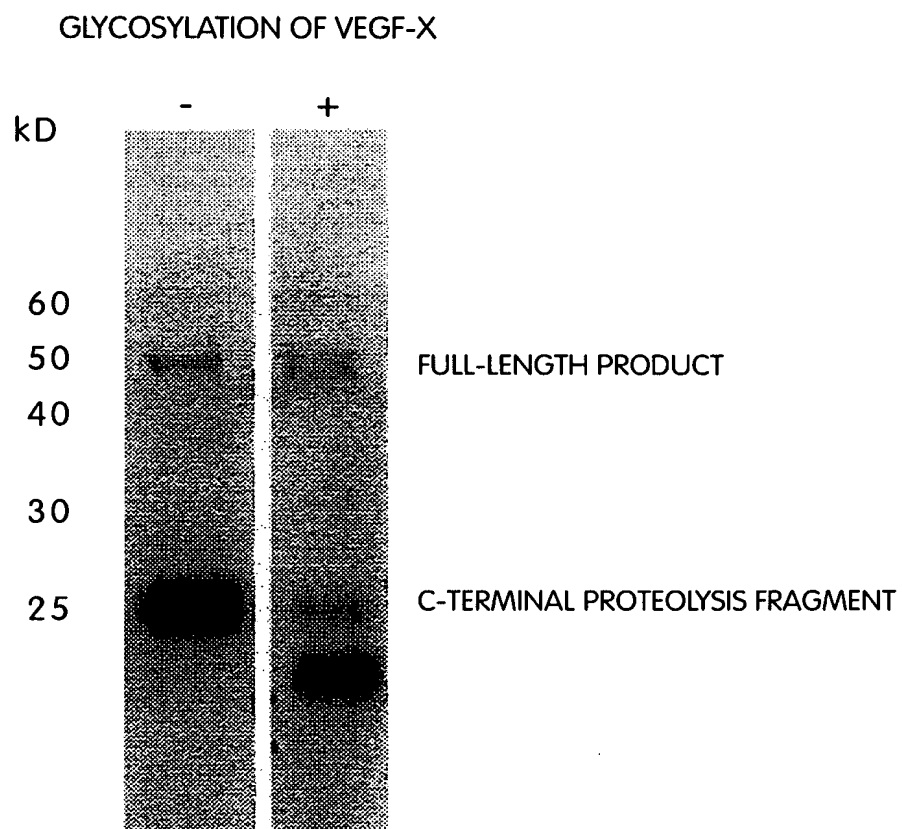


Fig. 23



VASCULAR ENDOTHELIAL GROWTH  
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DNA AND POLYPEPTIDE SEQUENCE USED FOR E.coli  
EXPRESSION OF THE PDGF-LIKE DOMAIN

```
+ 3           M R G S H H H H H H G M A S M
1  AAGGAGATAT ACATATGCGG GGTTCATCATC ATCATCATCA TCATGGTATG GCTAGCATGA

+ 3  T G G O O M G R D L Y D D D D K D P G R
61  CTGGTGGACA GCAAATGGGT CGGGATCTGT ACGACGATGA CGATAAGGAT CCGCGAAGAA

+ 3  K S R V V D L N L L T E E V R L Y S C T
121 AATCCAGAGT GGTGGATCTG AACCTTCTAA CAGAGGAGGT AAGATTATAC AGCTGCACAC

+ 3  P R N F S V S I R E E L K R T D T I F W
101 CTCGTAACCTT CTCAGTGTCC ATAAGGGAAG AACTAAAGAG AACCGATACC ATTTTCTGGC

+ 3  P G C L L V K R C G G N C A C C L H N C
241 CAGGTTGTCT CCTGGTTAAA CGCTGTGGTG GGAAGTGTGC CTGTTGTCTC CACAATTGCA

+ 3  N E C Q C V P S K V T K K Y H E V L Q L
301 ATGAATGTCA ATGTGTCCCA AGCAAAGTTA CTAAAAAATA CCACGAGGTC CTTTCAGTTGA

+ 3  R P K T G V R G L H K S L T D V A L E H
361 GACCAAAGAC CCGTGTGAGG CGATTGCACA AATCACTCAC CGACGTGGCC CTGGAGCACC

+ 3  H E E C D C V C R G S T G G
421 ATGAGGAGTG TGAAGTGTG TGCAGAGGGA GCACAGGAGG ATAATGAATT CGAAGCTTGA

481 TCCGGCTGCT AACAAAGCCC
```

Fig. 24



VASCULAR ENDOTHELIAL GROWTH  
FACTOR-X  
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EXPRESSION OF PDGF DOMAIN IN E.coli

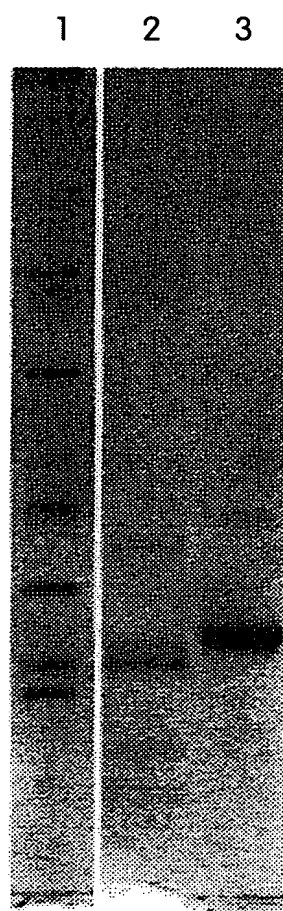


Fig. 25



VASCULAR ENDOTHELIAL GROWTH  
FACTOR-X

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DNA AND POLYPEPTIDE SEQUENCE USED FOR E.coli  
EXPRESSION OF THE CUB-LIKE DOMAIN

```
+ 2      M A M D I G I N S D P E S H H H H H H
1      GGCGATGGCC ATGGATATCG GAATTAATTC GGATCCGGAG TCTCACCATC ACCACCATCA

+2      E S N L S S K F Q F S S N K E Q N G V Q
61     TGAATCCAAC CTGAGTAGTA AATTCCAGTT TTCCAGCAAC AAGGAACAGA ACGGAGTACA

+2      D P Q H E R I I T V S T N G S I H S P R
121    AGATCCTCAG CATGAGAGAA TTATTACTGT GTCTACTAAT GGAAGTATTC ACAGCCCAAG

+2      F P H T Y P R N T V L V W R L V A V E E
181    GTTTCCTCAT ACTTATCCAA GAAATACGGT CTTGGTATGG AGATTAGTAG CAGTAGACGA

+2      N V W I Q L T F D E R F G L E D P E D D
241    AAATGTATGG ATACAACTTA CGTTTGATGA AAGATTTGGG CTTGAAGACC CAGAAGATGA

+ 2      I C K V D F V E V E E P S D G T I L G R
301    CATATGCAAG TATGATTTTG TAGAAGTTGA GGAACCCAGT GATGGAACTA TATTAGGGCG

+2      W C G S G T V P G K Q I S K G N Q I R I
361    CTGGTGTGGT TCTGGTACTG TACCAGGAAA ACAGATTTCT AAAGGAAATC AAATTAGGAT

+ 2      R F V S D E Y F P S E P G F C I H Y N I
421    AAGATTTGTA TCTGATGAAT ATTTTCCTTC TGAACCAGGG TTCTGCATCC ACTACAACAT

+2      V M P C F T E A V
491    TGTCATGCCA CAATTCACAG AAGCTGTGTA GTCGAGCTCC GTCGACAAGC TTGCGGCCCG

541    ACTCGAGCAC
```

Fig. 26



VASCULAR ENDOTHELIAL GROWTH  
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EXPRESSION OF THE CUB DOMAIN IN E.coli



Fig. 27

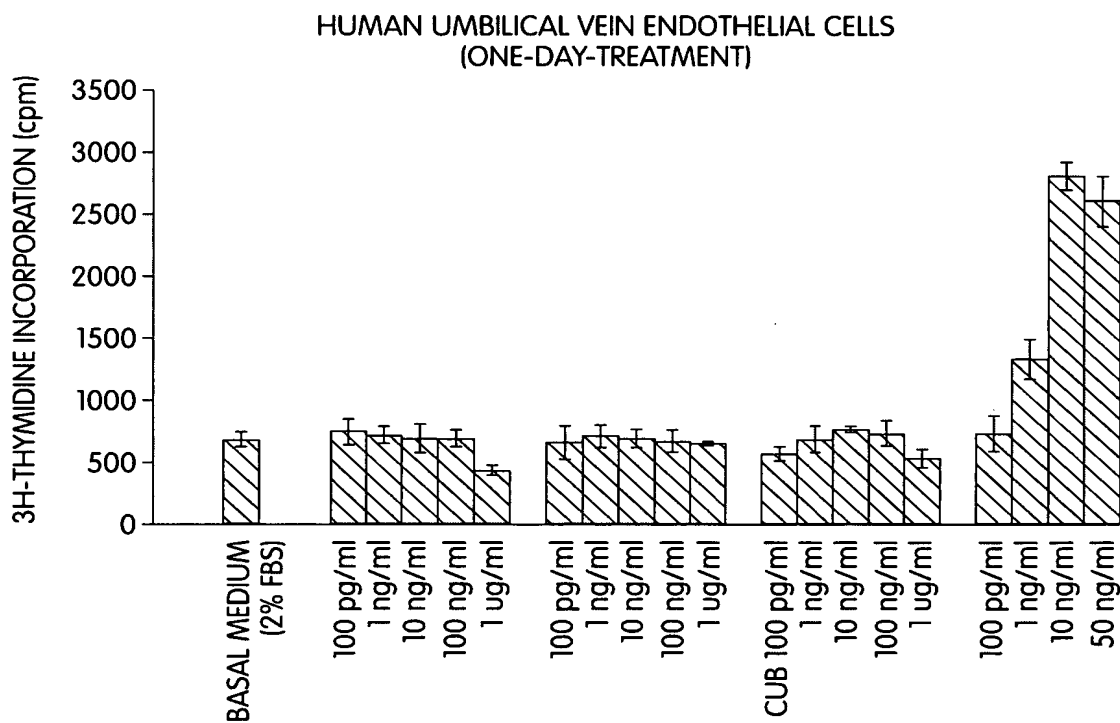


Fig. 28A



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HUMAN UMBILICAL VEIN ENDOTHELIAL CELLS  
(24-HOUR-STARVING FOLLOWED BY ONE-DAY-TREATMENT)

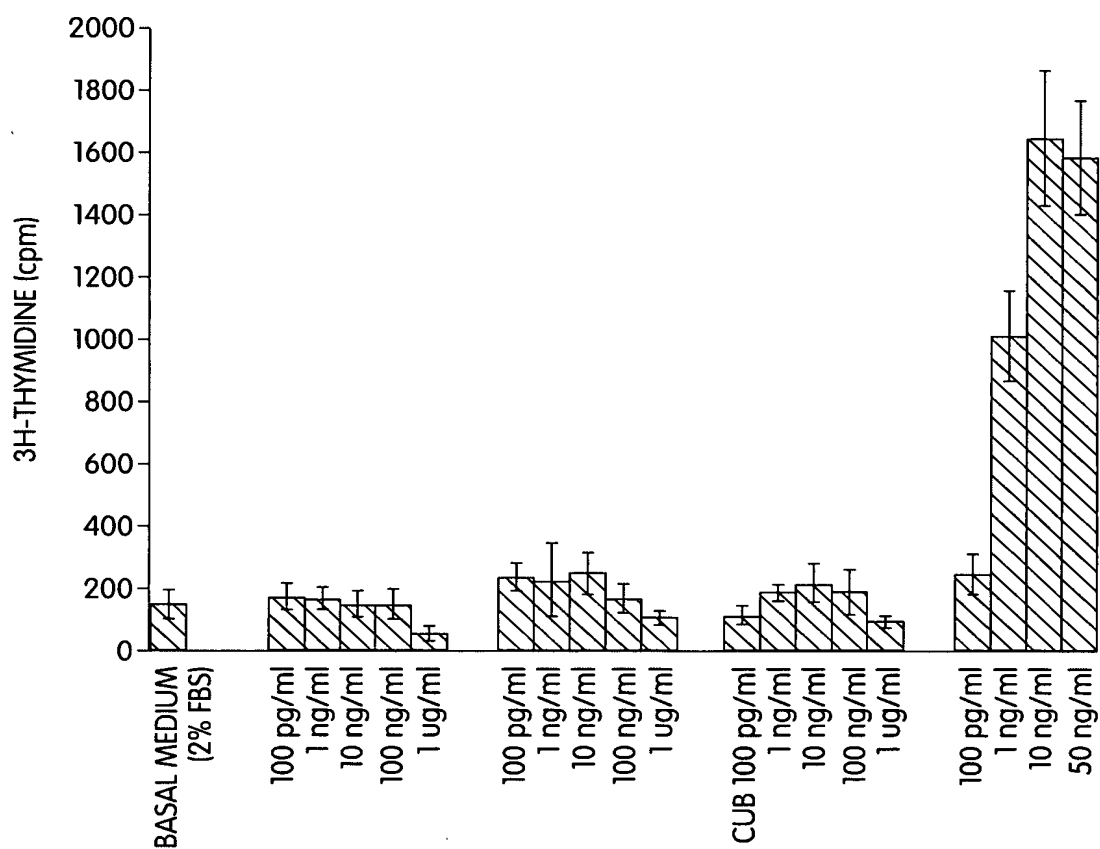


Fig. 28B



THE EFFECT OF VEGF-A<sub>165</sub> AND VEGF-X CUB DOMAIN  
ON THE PROLIFERATION OF HUVEC (TWO-DAY-TREATMENT)

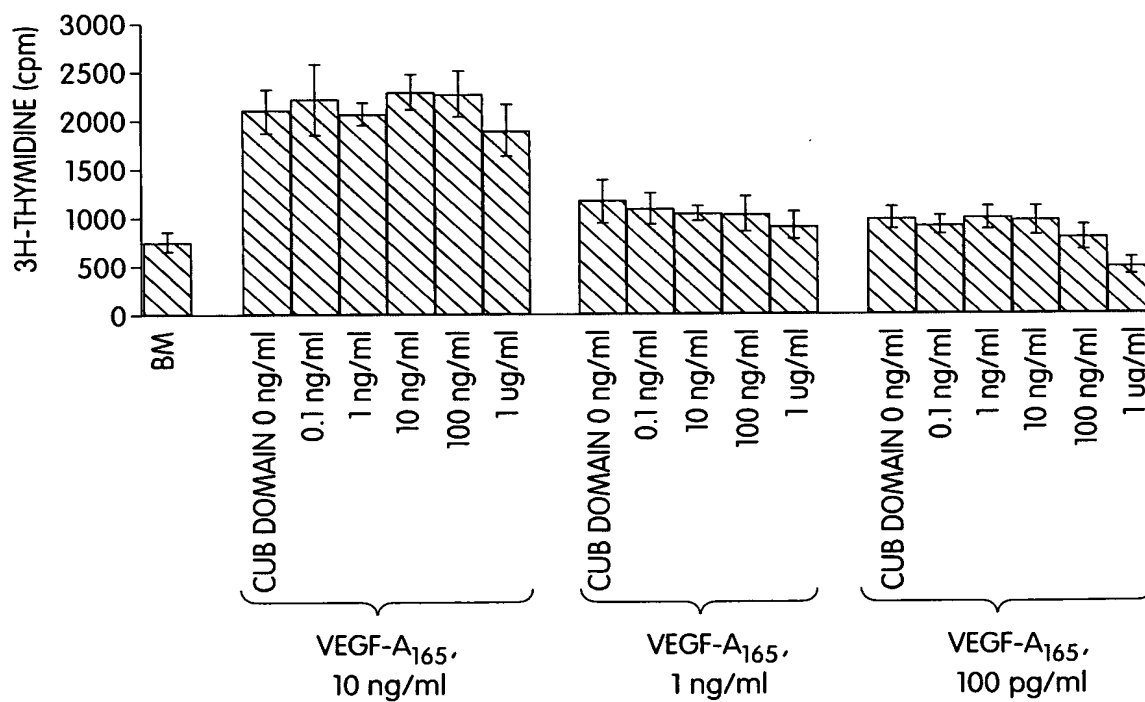
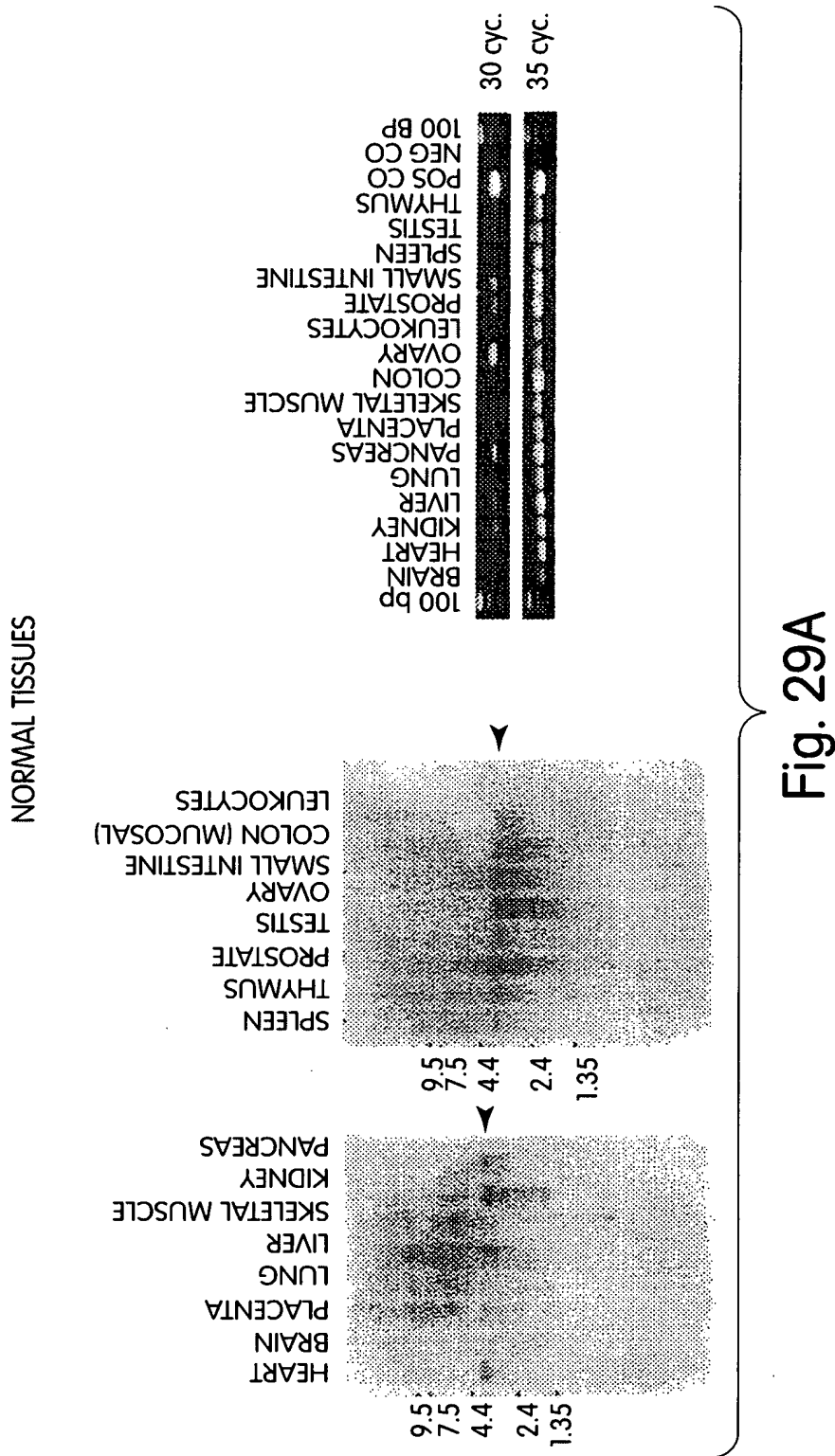


Fig. 28C





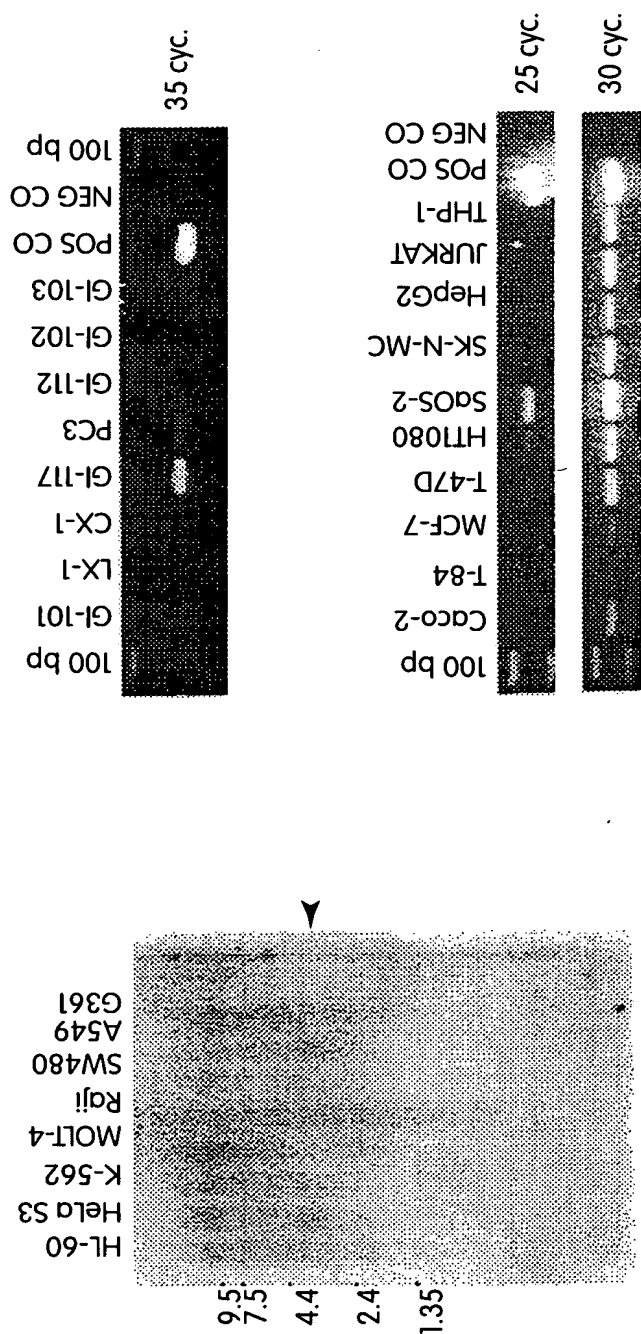
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TUMOR TISSUE AND CELL LINES







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LOCATION OF SPLICE SITES WITHIN THE cDNA SEQUENCE

1 GAATTCGCCC TTTTGTTTAA ACCTTGGGAA CTGGTTCAGG TCCAGGTTTT GCTTTGATCC  
61 TTTTCAAAAA CTGGAGACAC AGAAGAGGGC TCTAGGAAAA AGTTTTGGAT GGGATTATGT  
121 GGAAACTACC CTGCGATTCT CTGCTGCCAG AGCAGGCTCG GCGCTTCCAC CCCAGTGCAG  
181 CCTTCCCCTG GCGGTGGTGA AAGAGACTCG GGAGTCGCTG CTTCCAAAGT GCCCCCCGTG  
+3 M S L F G L L L L T S  
241 AGTGAGCTCT CACCCCAGTC AGCCAAATGA GCCTCTTCGG GCTTCTCCTG CTGACATCTG  
+3 A L A G Q R Q G T Q A E S N L S S K F Q  
301 CCCTGGCCGG CCAGAGACAG GGGACTCAGG CGGAATCCAA CCTGAGTAGT AAATTCCAGT  
+3 F S S N K E Q N G V Q D P Q H E R I I T  
361 TTTCCAGCAA CAAGGAACAG AACGGAGTAC AAGATCCTCA GCATGAGAGA ATTATTACTG  
+3 V S T N G S I H S P R F P H T Y P R N T  
421 TGTCTACTAA TGGAAGTATT CACAGCCCAA GGTTCCTCA TACTTATCCA AGAAATACGG  
+3 V L V W R L V A V E E N V W I Q L T F D  
481 TCTTGGTATG GAGATTAGTA GCAGTAGAGG AAAATGTATG GATACAACCTT ACGTTTGATG  
+3 E R F G L E D P E D D I C K Y D F V E V  
541 AAAGATTTGG GCTTGAAGAC CCAGAAGATG ACATATGCAA GTATGATTTT GTAGAAGTTG  
+3 E E P S D G T I L G R W C G S G T V P G  
601 AGGAACCCAG TGATGGAACCT ATATTAGGGC GCTGGTGTGG TTCTGGTACT GTACCAGGAA  
+3 K Q I S K G N Q I R I R F V S D E Y F P  
661 AACAGATTTT TAAAGGAAAT CAAATTAGGA TAAGATTTGT ATCTGATGAA TATTTTCCTT  
+3 S E P G F C I H Y N I V M P Q F T E A V  
721 CTGAACCCAG GTTCTGCATC CACTACAACA TTGTCATGCC ACAATTCACA GAAGCTGTGA  
+3 S P S V L P P S A L P L D L L N N A I T  
781 GTCCTTCAGT GCTACCCCTC TCAGCTTTGC CACTGGACCT GCTTAATAAT GCTATAACTG  
+3 A F S T L E D L I R Y L E P E R W Q L D  
841 CCTTTAGTAC CTTGGAAGAC CTTATTCGAT ATCTTGAACC AGAGAGATGG CAGTTGGACT  
+3 L E D L Y R P T W Q L L G K A F V F G R  
901 TAGAAGATCT ATATAGGCCA ACTTGGCAAC TTCTTGGCAA GGCTTTTGTGTT TTTGGAAGAA  
+3 K S R V V D L N L L T E E V R L Y S C T  
961 AATCCAGAGT GGTGGATCTG AACCTTCTAA CAGAGGAGT AAGATTATAC AGCTGCACAC

Fig. 30B-1



VASCULAR ENDOTHELIAL GROWTH  
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+3 P R N F S V S I R E E L K R T D T I F W  
1021 CTCGTAAGTCT CTCAGTGTCC ATAAGGGAAG AACTAAAGAG AACCGATACC ATTTTCTGGC

+3 P G C L L V K R C G G N C A C C L H N C  
1081 CAGGTTGTCT CCTGGTTAAA CGCTGTGGTG GGAAGTGTGC CTGTTGTCTC CACAATTGCA

+3 N E C Q C V P S K V T K K Y H E V L Q L  
1141 ATGAATGTCA ATGTGTCCCA AGCAAAGTTA CTAAAAATA CCACGAGGTC CTTCAGTTGA

+3 R P K T G V R G L H K S L T D V A L E H  
1201 GACCAAAGAC CGGTGTCAGG GGATTGCACA AATCACTCAC CGACGTGGCC CTGGAGCACC

+3 H E E C D C V C R G S T G G  
1261 ATGAGGAGTG TGACTGTGTG TGCAGAGGGA GCACAGGAGG ATAGCCGCAT CACCACCAGC

1321 AGCTCTTGCC CAGAGCTGTG CAGTGCAGTG GCTGATTCTA TTAGAGAACG TATGCGTTAT

1381 CTCCATCCTT AATCTCAGTT GTTTGCTTCA AGGACCTTTC ATCTTCAGGA TTTACAGTGC

1441 ATTCTGAAAG AGGAGACATC AAACAGAATT AGGAGTTGTG CAACAGCTCT TTTGAGAGGA

1501 GGCCTAAAGG ACAGGAGAAA AGGTCTTCAA TCGTGGAAAG AAAATTAAAT GTTGTATTAA

1561 ATAGATCACC AGCTAGTTTC AGAGTTACCA TGTACGTATT CCACTAGCTG GGTTCTGTAT

1621 TTCAGTTCTT TCGATACGGC TTAGGGTAAT GTCAGTACAG GAAAAAACT GTGCAAGTGA

1681 GCACCTGATT CCGTTGCCTT GCTTAACTCT AAAGCTCCAT GTCCTGGGCC TAAATCGTA

1741 TAAATCTGG ATTTTTTTTT TTTTTTTTGT CTCATATTCA CATATGTAAA CCAGAACATT

1801 CTATGTACTA CAAACCTGGT TTTTAAAAAG GAACTATGTT GCTATGAATT AAAGTTGTGT

1861 CATGCTGATA GGACAGACTG GATTTTTCAT ATTTCTTATT AAAATTTCTG CCATTTAGAA

1921 GAAGAGAAGT ACATTCATGG TTTGGAAGAG ATAAACCTGA AAAGAAGAGT GGCCTTATCT

1981 TCACTTTATC GATAAGTCAG TTTATTTGTT TCATTGTGTA CATTTTATA TTCTCCTTTT

2041 GACATTATAA CTGTTGGCTT TTCTAATCTT GTTAAATATA TCTATTTTTA CCAAAGGTAT

2101 TTAATATTCT TTTTATGAC AACTTAGATC AACTATTTT AGCTTGGTAA ATTTTCTAA

2161 ACACAATTGT TATAGCCAGA GGAACAAAGA TGATATAAAA TATTGTTGCT CTGACAAAA

2221 TACATGTATT TCATTCTCGT ATGGTGCTAG AGTTAGATTA ATCTGCATTT TAAAAAACTG

2281 AATTGGAATA GAATTGGTAA GTTGCAAAGA CTTTTTGAAA ATAATTAAAT TATCATATCT

2341 TCCATTCCTG TTATTGGAGA TGAAAAATAA AAGCAACTTA TGAAAGTAGA CATTGAGATC

2401 CAGCCATTAC TAACCTATTC CTTTTTTGGG GAAATCTGAG CCTAGCTCAG AAAACATAA

2461 AGCACCTTGA AAAAGACTTG GCAGCTTCCT GATAAAGCGT GCTGTGCTGT GCAGTAGGAA

2521 CACATCCTAT TTATTGTGAT GTTGTGGTTT TATTATCTTA AACTCTGTTC CATACTTGT

2581 TATAAATACA TGGATATTTT TATGTACAGA AGTATGTCTC TTAACAGTT CACTTATTGT

2641 ACCTGGAAGG GCGAATTCTG CAGATATC

Fig. 30B-2



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THE EFFECT OF FL-VEGF-X ON HUVEC PROLIFERATION:  
(24-HOUR SERUM STARVATION FOLLOWED BY ONE DAY-TREATMENT)

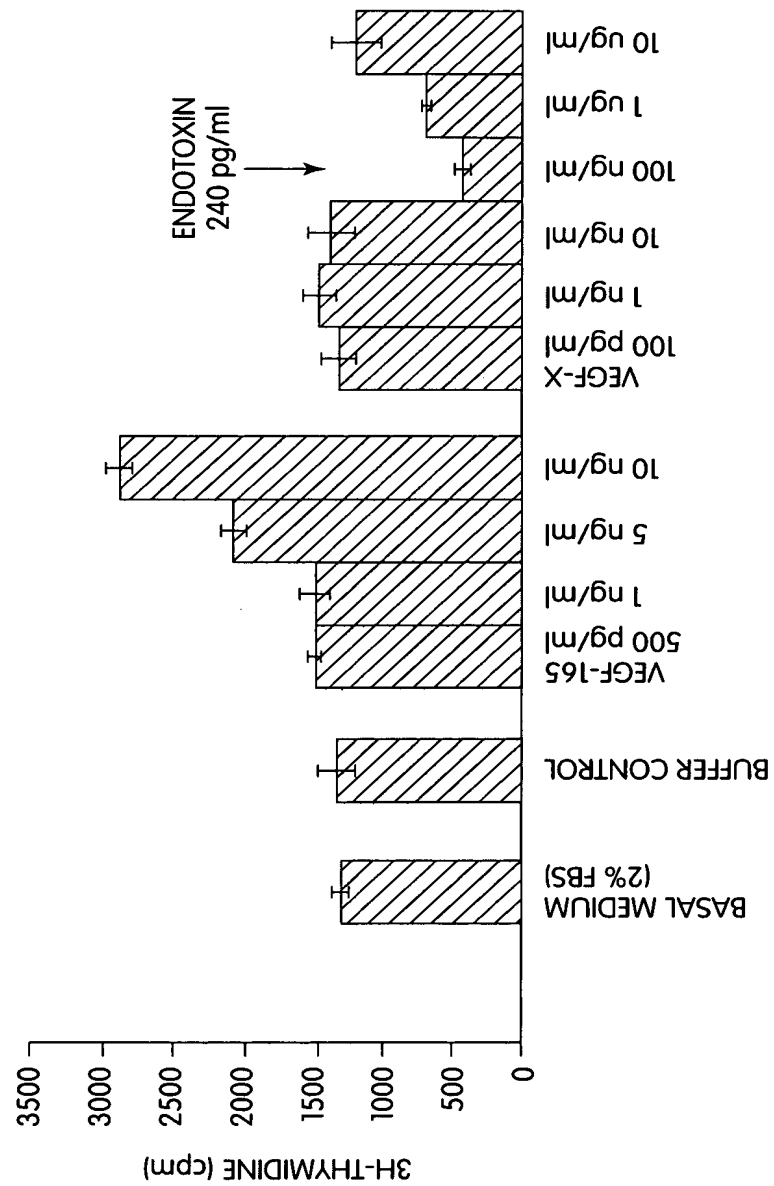


Fig. 31



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THE COMBINED EFFECT OF TRUNCATED VEGF-X (CUB DOMAIN) AND  
HUMAN RECOMBINANT VEGF<sub>165</sub> ON HUVEC PROLIFERATION:  
(24-HOUR SERUM STARVATION FOLLOWED BY TWO-DAY-TREATMENT)

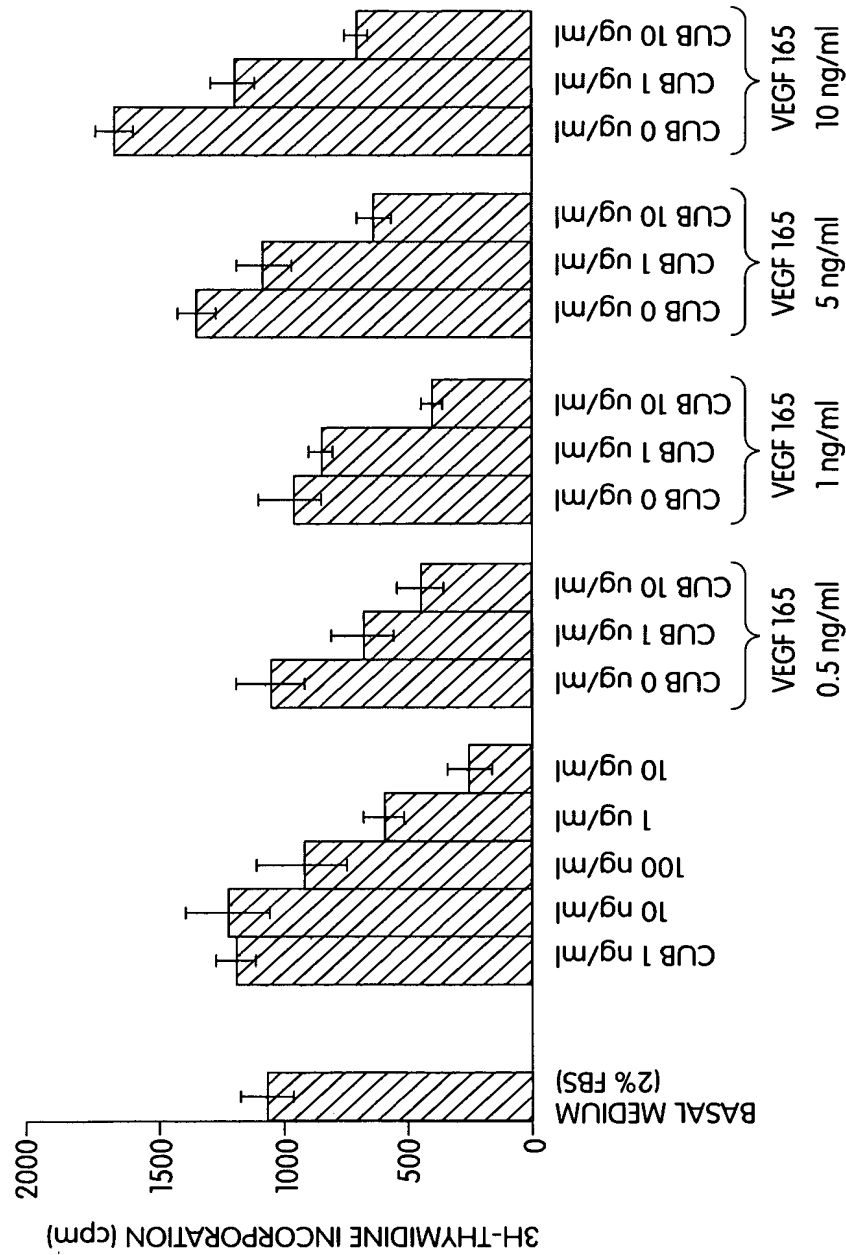


Fig. 32



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THE COMBINED EFFECT OF CUB DOMAIN AND HUMAN RECOMBINANT  
bFGF ON HUVEC PROLIFERATION:  
(24-HOUR SERUM STARVATION FOLLOWED BY TWO-DAY-TREATMENT)

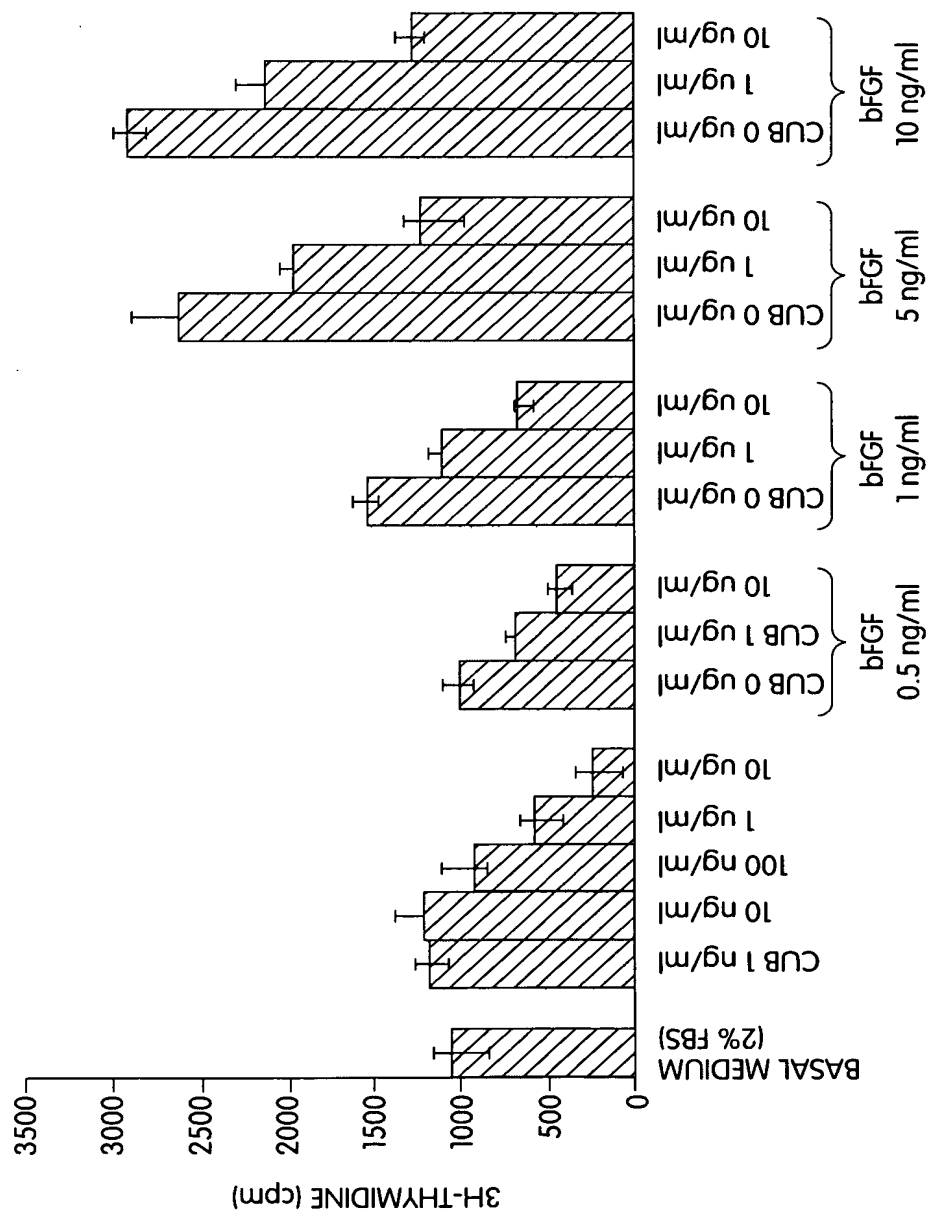


Fig. 33





LDH ASSAY FOR TESTING CYTOTOXICITY OF CUB DOMAIN  
OR CUB DOMAIN WITH rh VEGF<sub>165</sub>

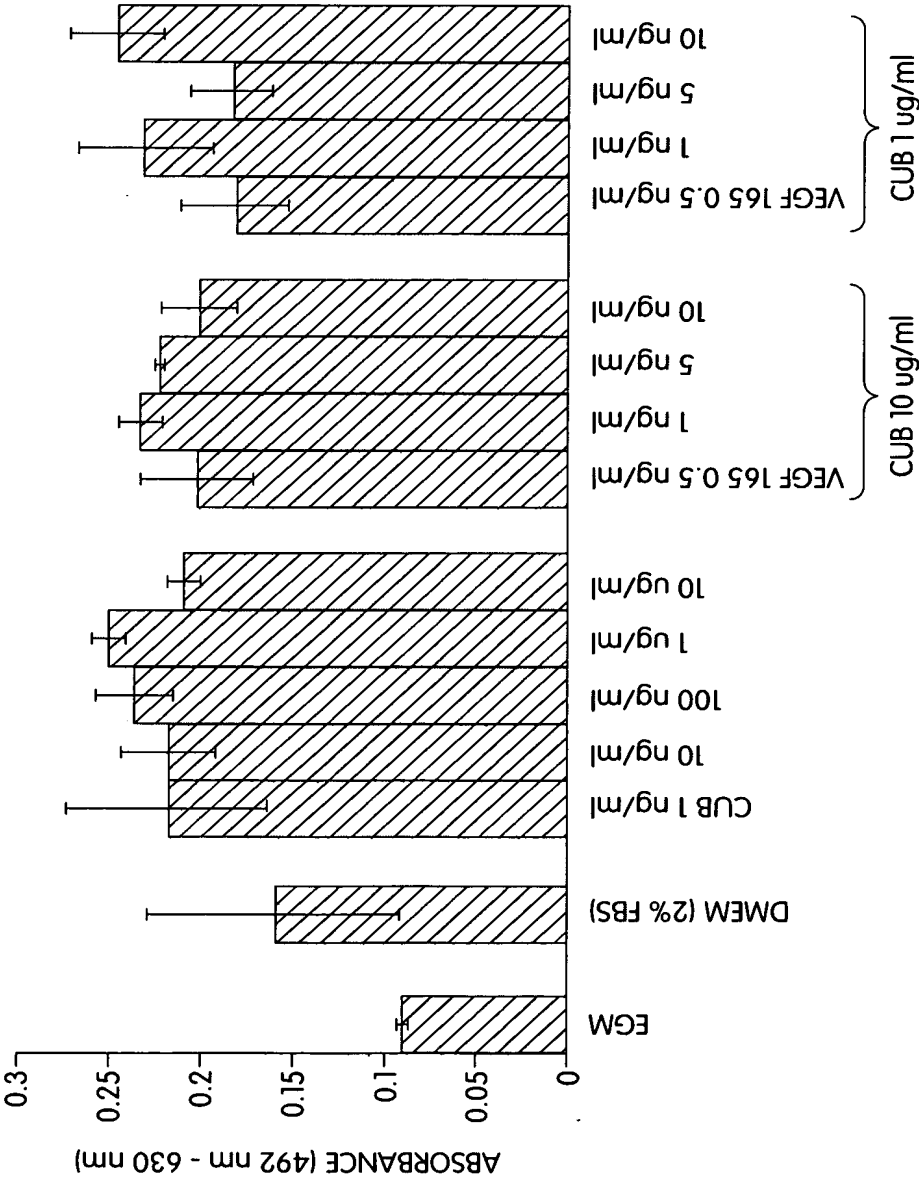


Fig. 34



66/66

LDH ASSAY FOR TESTING CYTOTOXICITY OF CUB DOMAIN  
OR CUB DOMAIN WITH rh-bFGF

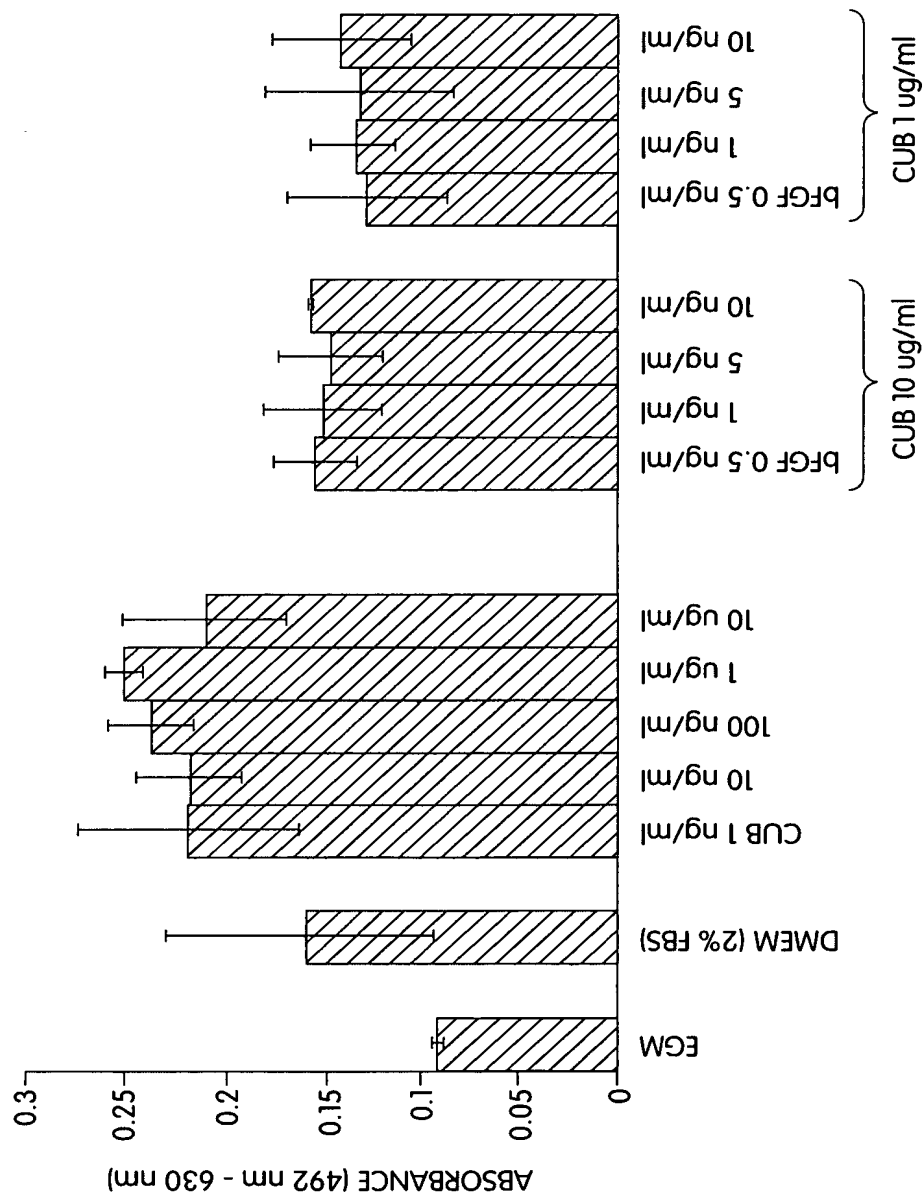


Fig. 35